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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:00:43 ; Search time 6808.06 Seconds
(without alignments)
16857.498 Million cell updates/sec

Title: US-10-782-141-2

Perfect score: 2019
Sequence: 1 gtagaaaatacgaatccta.....atagttattatcaatlaa 2019

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2019	100.0	2019	6	CQ868325 Sequence
2	2019	100.0	2145	6	CQ868324 Sequence
3	2010	99.6	2010	6	CQ868327 Sequence
4	949.2	47.0	3746	1	AB074414 Sequence
5	803.6	39.8	4100	1	AB112346 Sequence
6	747.2	37.0	2082	6	CQ868312 Sequence
7	747.2	37.0	5980	6	CQ868311 Sequence
8	739.8	36.6	2073	6	CQ868314 Sequence
9	214	10.6	3931	1	AB161456 Sequence
10	197.2	9.8	2028	1	BTU88189 Sequence
11	180.6	8.9	2028	1	BTU88188 Sequence
12	172.4	8.5	3468	6	AR143378 Sequence
13	172.4	8.5	3468	6	AR567184 Sequence
14	172.4	8.5	3471	6	BD062618 Toxin ac
15	172.4	8.5	3471	6	BD128371 Toxin act
16	172.4	8.5	3471	6	AR205863 Sequence
17	172.4	8.5	3471	6	AR339971 Sequence
18	172.4	8.5	3471	6	AR559861 Sequence

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20 172.4 8.5 3726 6 AR567185
21 172.4 8.5 3837 1 BTCRY1GL
22 172.4 8.5 12579 1 BTCRY1
23 162.8 8.1 2407 6 AR359378
24 162.8 8.1 2407 6 AX098659
25 147.4 7.3 3668 1 AB185105
26 133.6 6.6 4391 1 BTU8665
27 119.8 5.9 1959 6 AR359366
28 119.8 5.9 1959 6 AX098635
29 118.4 5.9 1986 6 CQ868322
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31 118.4 5.9 2049 6 CQ868318
32 118.2 5.9 3636 1 AY138457
33 118.2 5.9 3842 1 BTMCRYIBC
34 118.2 5.9 3934 1 BACCRYIE
35 118.2 5.9 3934 6 AR068828
36 118.2 5.9 3934 6 I38760
37 118.2 5.9 3934 6 I70138
38 118.2 5.9 8306 1 BTU70726
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40 117.6 5.8 1890 6 CQ868301
41 117.6 5.8 2190 6 CQ868300
42 116.8 5.8 2549 1 AY570734
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44 116.8 5.8 3684 6 I90319
45 116.8 5.8 3684 6 AR359400

ALIGNMENTS

RESULT 1
CQ868325 2019 bp DNA linear PAT 13-SEP-2004
LOCUS Sequence 26 from Patent WO2004074462.
DEFINITION CQ868325
ACCESSION CQ868325.1 GI:51998371
VERSION
KEYWORDS
SOURCE
ORGANISM
Bacillus thuringiensis
Bacillus thuringiensis
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus
cereus group.

REFERENCE
1 Carozzi N., Hargies T., Koziel M.G., Duck N.B. and Carr B.
AUTHORS
TITLE Delta-endotoxin genes and methods for their use
JOURNAL Patent: WO 2004074462-A 26 02-SEP-2004;
Athenix Corporation (US)
FEATURES
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/organism="Bacillus thuringiensis"
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ORIGIN

Query Match 100.0%; Score 2019; DB 6; Length 2019;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
CQ868324 2145 bp DNA linear PAT 13-SBP-2004
LOCUS CQ868324
DEFINITION Sequence 25 from Patent WO2004074462.
ACCESSION CQ868324

VERSION CQ868324.1 GI:51998370
KEYWORDS Bacillus thuringiensis
SOURCE Bacillus thuringiensis
ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1
AUTHORS Carozzi, N., Hargiss, T., Koziel, M.G., Duck, N.B. and Carr, B.
TITLE Delta-endotoxin genes and methods for their use
JOURNAL Patent: WO 2004/074462-A 25 02-SEP-2004;
Athenix Corporation (US)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	2107	ACAAAAAGAGATGTGTAATAGTTTATTTATCAATTAA	2145
RESULT 3			
LOCUS	C0868327	2010 bp	DNA linear PAT 13-SEP-2004
DEFINITION	Sequence 28 from Patent WO2004074462.		
ACCESSION	C0868327		
VERSION	C0868327.1	GI:51998373	
KEYWORDS			
SOURCE	Bacillus thuringiensis		
ORGANISM	Bacillus thuringiensis Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.		
REFERENCE	1		
AUTHORS	Carozzi, N., Hargies, T., Koziel, M.G., Duck, N.B. and Carr, B.		
TITLE	Delta-endotoxin genes and methods for their use		
JOURNAL	Patent: WO 2004/074462-A 28 02-SEP-2004; Athenix Corporation (US)		
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ORIGIN			
Query Match	99.6%	Score 2010; DB 6; Length 2010;	
Best Local Similarity	100.0%	Pred. No. 0;	
Matches 2010; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;	

QY	250	TCAATATTAACAACTGATTCGCTCTTGCTGATCTGTGGACGACTTTCTATATGT	309
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Db	301	GATTTAGTATCTATATTCGTAAAGAGGTAGACGAGACGCTGTAAAGACGGGTTGCA	360
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QY	430	CTTACAGATTAATCAAACTCTTAAACCTGCTGACGATGTTAAACATGTCACACG	489
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Oy		1330	CAGACAAATTGAATCTGTGTCACAGATTTTAATAAAGATCTAACCACTCAGTGCCTAACAT	1389
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LOCUS	AB074414			
DEFINITION	Bacillus thuringiensis serovar aizawai Cry40k and 40orf2 genes for putative mosquitocidal toxin and Cry40ORF2 protein, partial and complete cds.			
ACCESSION	AB074414			
VERSION	AB074414.1	GI:16945771		
KEYWORDS				
SOURCE	Bacillus thuringiensis serovar aizawai			
ORGANISM	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.			
REFERENCE	1 Ito,T., Sahara,K., Asano,S. and Bando,H. Cloning and Expression of Novel Crystall Protein Genes from Bacillus thuringiensis subsp. aizawai Encoding a Mosquitocidal Proteins Unpublished 2 (bases 1 to 3746)			
AUTHORS	Ito,T., Sahara,K., Asano,S. and Bando,H.			
JOURNAL	Direct Submission			
AUTHORS	Submitted (14-NOV-2001) Takeshi Ito, Graduate school of Agriculture,Hokkaido University, Kita-5Yyou Nishi-9chome, Kitak-Ku,Sapporo-shi, Hokkaido 060-8589, Japan			
TITLE	JOURNAL			
JOURNAL	JOURNAL			
AUTHORS	JOURNAL			
TITLE	JOURNAL			
JOURNAL	JOURNAL			

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FEATURES
(E-mail: lto-t@abs.agr.hokudai.ac.jp, Tel: 81-011-716-2487)

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ORIGIN
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Best Local Similarity 71.4%; Pred. No. 5,3e-173;
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RESULT 5
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 LOCUS 4100 bp DNA linear BCT 14-JUN-2003
 DEFINITION Bacillus thuringiensis serovar aizawai cry40-like and ORF2 genes for putative mosquitoicidal toxin, hypothetical protein, complete cds.
 ACCESSION AB112346 GI:31745043
 VERSION AB112346.1
 KEYWORDS Bacillus thuringiensis serovar aizawai
 SOURCE Bacillus thuringiensis serovar aizawai
 ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
 AUTHORS Ito, T., Sahara, K., Asano, S. and Bando, H.
 TITLE Cloning and Expression of Novel Crystal Protein Genes from Bacillus thuringiensis subsp. aizawai Encoding Mosquitoicidal Proteins
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 4100)
 AUTHORS Ito, T., Sahara, K., Asano, S. and Bando, H.
 TITLE Direct Submission
 JOURNAL Submitted (12-JUN-2003) Takeshi Ito, Graduate School of Agriculture, Hokkaido University, Department of Applied Bioscience, Kita-9-jo, Nishi-9chome, Kita-ku, Sapporo, Hokkaido 060-8589, Japan

(E-mail: hco-t@abs.agr.hokudai.ac.jp, Tel: 81-11-706-2487 (ex. 2487))

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450 ACAGATATGAGGATGATCTTATTAATTTCTTGGAGAACCTTACATTAATCGGATCAAT 509
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 DEFINITION Sequence 12 from Patent WO2004074462.
 ACCESSION CO868311
 VERSION CO868311.1 GI:51998357
 KEYWORDS
 SOURCE Bacillus thuringiensis
 ORGANISM Bacillus thuringiensis
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
 1 Carozzi, N., Hargiss, T., Koziel, M.G., Duck, N.B. and Carr, B.
 Delta-endotoxin genes and methods for their use
 Patent: WO 2004074462-A 12 02-SEP-2004;

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 Best Local Similarity 69.8%; Pred. No. 4,4e-134;
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 QY 301 TCTAATGATTAATTAATTAATTCGTAAGAGGTAGACAGAGCGTTTAAGTAC 360
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 QY 361 GGGGTTCAGATTTTGAAGGTGAATGATCTGTTATCAAGATTAATTTCTTCAATATCTT 420
 Db 528 GCGATTTGCAATTTTGAAGGTGAATGATCTGTTATCAAGATTAATTTCTTCAATATCTT 587
 QY 421 GAGATTTGGCTACAG-----ATTAATCAATCTTAATAAACTTGCGAC 465
 Db 588 GGGCTTTGGCTTAAGACGTTAAACCTTCAAAACCAATTAATCTGATATGAGCA 647
 QY 466 GTAGTTAAACAGTTCACAGACGGAAGATTTCTAATCTTTTACAGAGGTCAATTA 525
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 QY 526 TCAAGACAGAAAGCTGAATATTTATTTTTCCTACGATATGCAAGCTGCAATTTGAT 585
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 QY 586 TTATTTCTAATTAAGGAGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 645
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Db 1710 ACACAAATACCGGCGGTGAAGAGTTTATTAACCTTCAAAATTAATCTTGAATGCTTATACC 1769
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Db 1770 TATGTATTAATAAGGCACT 1787

RESULT 8
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LOCUS CQ868314 2073 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 15 from Patent WO2004074462.
ACCESSION CQ868314
VERSION CQ868314.1 GI:51998360
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
AUTHORS Carozzi,N., Hargies,T., Koziel,M.G., Duck,N.B. and Carr,B.
TITLE Delta-endotoxin genes and methods for their use
JOURNAL Patent: WO 2004074462-A 15 02-SEP-2004;
Athenix Corporation (US)
FEATURES
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ORIGIN
Query Match 36.6%; Score 739.8; DB 6; Length 2073;
Best Local Similarity 69.7%; Pred. No. 1.6e-132;
Matches 1135; Conservative 0; Mismatches 422; Indels 72; Gaps 7;
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Qy 70 AATATGTCAACAGATATCTTTTGGCAAGAGATCCAAATATATTTCTTAACTGAC 129
Db 61 AATAGCCCAACAGATATCTTTTGGCAAGAGATCCAAATATATTTCTTAACTGAC 120
Qy 130 GCTTGTACAGGAAAGCCATGCAAGATACGTGGAAATGCTTCGGAATAGTAATTT 189
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Qy 190 GGGACATACCTTATTCATTTCTGTAGAACCCGGATATGAGGAAATTCCTGTAATTT 249
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 DEFINITION Bacillus thuringiensis serovar entomocidus cry4Ba like and ORF2
 complete cds.
 ACCESSION AB161456
 AB161456.1 GI:41688282

KEYWORDS
 SOURCE Bacillus thuringiensis serovar entomocidus
 ORGANISM Bacillus thuringiensis serovar entomocidus
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
 REFERENCE
 1 Ikeya, T., Yamaya, K., Ito, T., Sahara, K., Bando, H. and Amano, S.
 Cloning and Expression of Novel Crystal Protein Genes from Bacillus thuringiensis subsp. entomocidus INA288
 Unpublished
 2 (bases 1 to 3931)
 AUTHORS Tomonori, I., Kumiko, Y., Takechi, I., Ken, S., Shin-ichiro, A. and Hisanori, B.
 TITLE Direct Submission
 JOURNAL Submitted (30-JAN-2004) Ikeya Tomonori, Graduate School of Agriculture, Hokkaido University, Department of Applied Bioscience; Kita-9jo, Nishi-9choe, Kita-ku, Sapporo, Hokkaido 0608589, Japan (E-mail: ikeyanabe.agr.hokudai.ac.jp, Tel:81-011-706-2487(ex.2487), Fax:81-011-706-2487)

FEATURES
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ORIGIN

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Db 1945 TTTAAATATTAGAACTTATCTGATCACTTTAATAATATCTGTTGAAATAATTAATA 2004
Qy 1849 CAATACTATCTGTTACACCTTATGTTGACAAAGTCAATTTTCCCAATTGACA 1906
Db 2005 CAATACTATCTGTTGCAACTTATCTGTTGACAACTGTAATTTATCCCAATTGAAA 2062

RESULT 10
LOCUS BTU88189 2028 bp DNA linear BCT 01-OCT-1998
DEFINITION Bacillus thuringiensis jegathesan insecticidal protein Jegg74 gene,
complete cds.
VERSION U88189
KEYWORDS U88189.1 GI:3668334
SOURCE Bacillus thuringiensis serovar jegathesan
ORGANISM Bacillus thuringiensis serovar jegathesan
Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus; Bacillus cereus group.
1 (bases 1 to 2028)
Kawalek, M.D. and Gill, S.S.
Isolation and characterization of insecticidal genes from Bacillus thuringiensis subsp. jegathesan
Unpublished
2 (bases 1 to 2028)
Kawalek, M.D. and Gill, S.S.
Direct Submission
Submitted (29-JAN-1997) Entomology, University of California, 5419
Boyce Hall, Riverside, CA 92521, USA
Location/Qualifiers
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IREVGPITTSADPSESEFLKIKITDHCISYIDGLAKISRSDSDETWENFKP
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Query Match 9.8%; Score 197.2; DB 1; Length 2028;
Best Local Similarity 54.6%; Pred. No. 7.4e-28;
Matches 524; Conservative 0; Mismatches 398; Indels 38; Gaps 5;
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Qy 10 ATGAATTCCTTATCAAAATATCAAAATGAATGAATTCGATGTTCCCGAATTAACA 69
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Qy 70 AATATGTCAACAGATATCCCTTTTCCAAAGATCCAAAT-----ATATTTCC 116
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Qy 117 TATTAACCTGACGCTTGTCAAGGAAGCCATGCAAGATACGTGGAAATCAGTCCGA 176
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Qy 177 TATTAAGATATGGAACATATACCTTATACAAATCTTGTGTAAGACCCGATATAGTGAAT 236
Db 181 GTTCTAGCAAGATATGTAATTTCTATTAATCTTGTCTACAGAGTCTTCCATAGAGAC 240
Qy 237 TCTGTATATTTTCAATTAATAACAATCTATCCGCTTGTGCAATCTGTGACAC 296
Db 241 GCAATTTGCTTTATGTAAGTCTATTTGAGAGATTTGGCCGAGACAGAACCTCGTTCC-C 299
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Qy 579 TGTGATTTATTAATTAAGGACGCAATTAATTAATAAAGATGGGACTAGTGTG 638
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Qy 639 TCCACCGTTGATCCAGGGTCAGGGAAGCTGA-----TTGTAACGAGCGGTTAAAGC 692
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Db 720 GCGTATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 779
Qy 753 AAGACAGGCGGTACAGATGCTGAAGATTGTCGAAATTAATTAATTTCTGAGGAAT 812
Db 780 AGTTCACAGGTTCAAGATGTTGAACCTTGTGGAGTGAATTTGATGAGAGAT 839
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LOCUS	BTU08188	
DEFINITION	Bacillus thuringiensis jegathesan insecticidal protein Jegt72 gene,	
ACCESSION	U08188	
VERSION	U08188.1	GI:3668332
KEYWORDS		
SOURCE		
ORGANISM	Bacillus thuringiensis serovar jegathesan Bacillus thuringiensis serovar Jegathesan Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.	
REFERENCE	1 (baes 1 to 2024) Kawalek,M.D. and Gill,S.S. Isolation and characterization of insecticidal genes from Bacillus thuringiensis subsp. jegathesan Unpublished	
AUTHORS	2 (baes 1 to 2024) Kawalek,M.D. and Gill,S.S. Direct Submission Submitted (29-JUN-1997) Entomology, University of California, 5419 Boyce Hall, Riverside, CA 92521, USA	
TITLE		
JOURNAL		
FEATURES	Location/Qualifiers	
Source	1..2024	
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Dn	71 ATATGTCAAACAGATATCCTTTTGCAAAAGATCCAAATATATTTCTATTAA----- 122	
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Dn	122 ATAAAGATTGGGTGATGATGATGAGGAAGGAATATATTTCTTCCTTCTCGCACAGAGA 181	
Dn	177 TATAGTAATCTATGGGACATACCTTATACAAATCTTGCTAGAACCCGGTATAGGTGAAT 236	
Dn	182 TAACTTCAAGATGTAATGATATGATGAAACCTTGCTAAAGCTGTACACTTCTC 241	
Dn	237 TCCTGTATATTTTCAATTAATAAC---AAATCATTCCTGCTTGTGTCATATCTGG 292	
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Qy	293	CAGACATTTCTAATGTGATTTAGTATCTAATAATTCCTAAAGAGGTGACAGACGGCTGT	352
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Qy	413	ATTATCTTGAGGATTTGGCTTACAGATTAATCAATTCCTAAABAACTTGCGAGCTAGTA	472
Db	422	GCCTCTGGAAAGCTTGAATTAACAATAAAGTAATTAATTAATACACAGAAACCTTGG	481
Qy	473	AACAGTTTCCAAGCAGGGAAAGAAAGATTTCACTAAACTTTTAGCGGGCTATTATCAAGAC	532
Db	482	AGGGCTTTAAGACTGTTGAAAGAGAAATTTTTCACAAAATTAAGATTAATATGAACTT	541
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Qy	773	CTGAAGTTTGGTCSAAATTTTAATTAATTTCTGTAGAGAAATGACGTTGGCGGTATGGATA	832
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Db	812	TAGTTTGGATATTTCCCAATTAATTAATCTGTTCGATATTCATTTATCGACAAAAATTTTCAC	871
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DEFINITION		Sequence 9 from patent US 6204246.	
ACCESSION		ARI43378	
VERSION		ARI43378.1	GI:15104664
KEYWORDS		Unknown.	
SOURCE		Unknown.	
ORGANISM		Unclassified.	
REFERENCE		1 (bases 1 to 3468)	
AUTHORS		Boech,H.Jan. and Stiekema,W.Johannes.	
TITLE		Hybrid toxin	
JOURNAL		Patent: US 6204246-A 9 20-MAR-2001;	
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REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

FEATURES

ORIGIN

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 3471)
Schnepf, E.H., Wicker, C., Narva, K.E., Walz, M. and Stockhoff, B.A.
Toxins active against pests
Patent: JP 2001507208-A 42 05-JUN-2001;
MYCOGEN CORP
JP 2001507208-A/42
PD 05-JUN-2001
PI ERNEST H SCHNEPF, CAROL WICKER, KENNETH E NARVA, MICHELE WALZ, PI
BRIAN A STOCKHOF
PC C12N15/32, C12O1/68, C12N15/82, C07K14/325, A01N63/00, A01H5/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

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221 CCGGATAGGTGGAATTCCTGTAATATTTT-----CAATAATAACAACATCTCCGT 274
218 CTCTCTTACTGATTAATTTCAATAGTATAGCCTTAGGTAAGTACTAGAGGTA 277
275 CTTCGTGATCTGTCGACGACCTTCTATATGTCATTTAGTATCTATATTCGTAAG 334
278 GTAGTGCACATCATATACAGATTTGCTATATGTCATTAATTAATTAATTTGATTAC 337
335 AGGTAGACGAGCGTGTATAGTACGCGGGTGCAGATTTGAGGGAATGACGCTT 394
338 GGGTAAGTCAGAGTGTTTTAAATGATGGGATTCAGATTTTAAATGTTCTGACTCTTAT 397
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440 AATCAATCTTAATAAACTGTCGACGTAATTAACAGTTCACAGCAGGAAAGAGATT 499
458 AAGAACTCCGTAATCTGTTTAAATGCGCAGCTCAGATTTGATAGATTTTAAACCGAG 517
500 TCACTAACTTTAGCAGGCTCATTTATCAAGAGGAAAGGTAATTTATTTATGCGTA 559
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620 AAGAAATGGGACATAGTGTCCACCGTTGATCCAGGGTCAAGGAAACGATTTGTAAG 679
638 CTAATTTGGGGCTATACATGCTACACCTTTTATA-----ATTATCAAT 682
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683 CAAATCTAGTAGCTTATTAAGTATTAATCTGATTTTTCGTAATGATTAATTCAG 742
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Db 863 TTACTATTAATCCCAATAGAAACGATTTTCAGTTGATGAGGTCATTTATACAGATCCA 922
Qy 920 TGGATATTCAGGGGGAATTAATGTTGGAA 951
Db 923 TTGTTTGTGATCATGCTAGTACTTGAAGGGA 954

RESULT 15
BD128371 3471 bp DNA linear PAT 18-SEP-2002
LOCUS
DEFINITION
Toxin active on Oestrinianubialis.
BD128371
ACCESSION
BD128371.1 GI:23223316
VERSION
BD128371.1 GI:23223316
KEYWORDS
JP 2002500166-A/42.
SOURCE
unidentified
ORGANISM
unidentified
unclassified.

REFERENCE
AUTHORS
TITLE
JOURNAL

Schnepf, E.H., Wicker, C., Narva, K.E., Walz, M., Stockhoff, B.A. and
Cohn, J.M.
Toxin active on Oestrinianubialis
Patent: JP 2002500166-A 42 08-JAN-2002;
MYCOGEN CORP
OS Unidentified
PN JP 2002500166-A/42
PD 08-JAN-2002
PR 15-DEC-1998 JP 2000526647
PR 31-DEC-1997 US 09/002285
PI ERNEST H SCHNEPF, CAROL WICKER, KENNETH E NARVA, MICHELE WALZ, PI
BRIAN A STOCKHOF, JUDY MULLER COHN
PC A01N63/02//C07K14/325, C12N15/09, C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Toxin active on Oestrinianubialis
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Location/Qualifiers
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ORIGIN

Query Match 8.5%; Score 172.4; DB 6; Length 3471;
Best Local Similarity 54.2%; Pred. No. 3.9e-23;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

161 GGGAAATCAGTCTCGGATATAGTAACTATTGGGACATCTTATACATCTTGGTAGAAC 220
158 GCGATGACGAAAGAGAGAGATATCTATTTGGACACCATAGCTCTCTTATACAGCAC 217
221 CCGGATAGGTGGAATTCCTGTAATATTTT-----CAATAATAACAACATCTCCGT 274
218 CTCTCTTACTGATTAATTTCAATAGTATAGCCTTAGGTAAGTACTAGAGGTA 277
275 CTTCGTGATCTGTCGACGACCTTCTATATGTCATTTAGTATCTATATTCGTAAG 334
278 GTAGTGCACATCATATACAGATTTGCTATATGTCATTAATTAATTAATTTGATTAC 337
335 AGGTAGACGAGCGTGTATAGTACGCGGGTGCAGATTTGAGGGAATGACGCTT 394
338 GGGTAAGTCAGAGTGTTTTAAATGATGGGATTCAGATTTTAAATGTTCTGACTCTTAT 397
395 ATCAAGATTATTAATCTTC-----ATTATCTTGAGGATTGGCTTACAGATA 439
398 ACAGAACTATTATTAAGAGCTCTGATAGTGAATAGATTCCTAATTCGCTTCTGCTG 457

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:00:54 ; Search time 5407.27 Seconds

(without alignments)
17469.639 Million cell updates/sec

Title: US-10-782-141-2

Sequence: 1 gtcgaaataatgtaattctta.....atagttattatcaattaa 2019

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hic.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gss81.*
10: gb_gss82.*
11: gb_gss83.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	65.2	3.2	1101	10	CNS0039G
C 2	56.2	2.8	1101	10	AL108811 Drosophila
C 3	53.6	2.7	1101	10	CNS0182P
C 4	53	2.6	1101	10	AL065414 Drosophila
C 5	51.8	2.6	1101	10	AL088379 Drosophila
C 6	51.4	2.5	1204	10	CNS01652
C 7	50.6	2.5	928	10	CNS0161D
C 8	49.6	2.5	1101	10	CNS0102F
C 9	48.4	2.4	938	10	CNS0006T
C 10	48.2	2.4	1101	10	CNS0106X
C 11	47.2	2.3	1101	10	CNS00100
C 12	46.6	2.3	867	11	CNS0758G
C 13	46.4	2.3	572	3	BP256971
C 14	46	2.3	355	1	AA448366
C 15	46	2.3	511	6	CB158772
C 16	46	2.3	817	5	BU773209
C 17	46	2.3	1414	4	BC025177
C 18	46	2.3	7050	10	AY420513
C 19	45.8	2.3	764	9	BZ025901
C 20	45.4	2.2	858	8	DR732187
C 21	45.4	2.2	1101	10	CNS017KX
C 22	45.2	2.2	350	10	N97363

23	45.2	2.2	583	9	BH725336	BH725336
24	45.2	2.2	1073	1	AJ928975	AJ928975
C 25	45	2.2	572	11	CR332988	CR332988
C 26	44.6	2.2	1092	10	CNS020K7	AL175696 Tetradon
C 27	44.6	2.2	1192	11	CNS03Y36	AL265803 Tetradon
C 28	44.4	2.2	550	5	BU778710	BU778710 JREG804
C 29	44.4	2.2	559	5	BU777332	BU777332 SUBD09
C 30	44.4	2.2	679	4	AY809710	AY809710 Schistoso
C 31	44.4	2.2	681	7	CV697396	CV697396 SUS_031_5
C 32	44.4	2.2	834	4	AY811172	AY811172 Schistoso
C 33	44.4	2.2	875	4	AY914981	AY914981 Schistoso
C 34	44.4	2.2	1001	10	CNS0155H	AL105023 Drosophila
C 35	44.2	2.2	639	9	BZ836800	BZ836800 CH240_258
C 36	44.2	2.2	1031	10	CNS000C2	AL059199 Drosophila
C 37	44	2.2	435	3	BJ015872	BJ015872 BJ015872
C 38	43.8	2.2	698	9	BH940326	BH940326 odg39c04.
C 39	43.8	2.2	918	10	CNS006MW	AL065768 Drosophila
C 40	43.6	2.2	387	5	BU495119	BU495119 PESTcab8
C 41	43.6	2.2	424	5	BQ56758	BQ56758 PESTcab2
C 42	43.6	2.2	583	5	BU498079	BU498079 PESTcab9
C 43	43.6	2.2	749	7	CK286885	CK286885 EST749607
C 44	43.6	2.2	790	10	CM496443	CM496443 feb001f2
C 45	43.6	2.2	840	9	AZ685747	AZ685747 ENTLW94TR

ALIGNMENTS

RESULT 1
LOCUS CNS0039G/c 1101 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL063921 GI:4941778
VERSION AL063921.1
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)

REFERENCE
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ooeogawa and Aaron Mammoeer in Pieter de Jong's laboratory in the department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pi and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source
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ORIGIN

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Qy	231	TGGAATTCCTGTAATATTTTCAATPATATAACAACTCATTCCTGTCGTGTCATCTGT	290	
Db	1072	KDRADRRMAGDADRMAMDDGAGTWTATATTTTMMWMMWMTWTPTWMDKMMWMTAAKTPTAM	1013	
Qy	291	GGCAGCATTCTCTATATGTGATTTAGTATCTATATTTGTTAAGAGGTAGACGAGCGCT	350	
Db	1012	TWMTATMRADWAGDRGAKKDRAPATADAGRRDGGRRKDKDRDXDGDGDKKGGK	953	
Qy	351	GTTAAGTGCAGCGGGTTCAGATTTTGAAGGTGAATGACCTGCTTCAAGATTTATATCT	410	
Db	952	KAABAARATATWMDWMDWMDKMKMDGACDKRADDDGADKDDKGDADDDDTGTCD	893	
Qy	411	TCATTTATCTTGAGGATTTGGCTTACAGATTAATCAATCTCAAAAACTTGCTGACGTAGT	470	
Db	892	DDKDKMDDMDKAKGTWGDATWAMAAATDMMWGMADADWMTDAAADDWMDRMDAMWK	833	
Qy	471	TAAACAGTTCACAGACGGGAAAGATTTCACTTAACCTTTTAGCAGGCTATTATCAAG	530	
Db	832	WDDAMWAGATPADRRDWGDRAGKRGAKRRDRKRADRKDAADRDPAATWTTWTTT	773	
Qy	531	ACAGAAAGCTGAATATATTTATTTGCTTACGATGTGCAAGCTGCAAGTGCATTTAT	590	
Db	772	RDTDDMKKXIDTWTMRMADRTWDRDDDDDRBAGTAGKMKRTMKRRKRDRTRDDDA	713	
Qy	591	ACTATTTAAGGACGACGATTAATATTAATAAAGAAATGGGACCTAGTGTCCACCGTTGA	650	
Db	712	DDTARDDBRRRGDDOAGDAGKGGKTKGRRRRBRATWRTDAMWMDAAWTTTDTDDMD	653	
Qy	651	TCCAGGCTCAGGGA--GACTGATTGTATACGACCGGTTTAAAGCAAAATTAAGAGTAT	708	
Db	652	KDRRRKARRRRTTAAAMDWTWTKAMDAKMKWTKRARMDWADTWTDAKARD	593	
Qy	709	ACTAATATTTGTAGAGGGTGAATTAACAAGGGTTAGATTCAGTAGACAGCGGGTACA	768	
Db	592	WAKRPMARARDRAPAADRRMTWKGTATTATWTTAPRAAAMWMAATTTATWTTT	533	
Qy	769	AGTCCTGAAGTTTGGTCGAAATTTAATAAATTTTCGTAGAGAATACCGTGGCGTATG	828	
Db	532	TTTWTTTTTTTTTTTTTTAAAMWMAATTAATAAATAAATAAATAAATTTTTTTTT	473	
Qy	829	GATATTTATGCTATATTTTCCAACTTATGATTTTGAATAATAT 870		
Db	472	TTWMTAAAMWTATWTTTWTTTTWTWMAATTTTTTTWTTW 431		
RESULT 2				
CNS0182P	1101 bp	DNA	linear	GSS 26-JUL-1999
LOCUS	Drosophila melanogaster genome survey sequence SP6 end of BAC			
DEFINITION	BACN37D10 of DrosBAC library from Drosophila melanogaster (fruit			
ACCESSION	fly), genomic survey sequence.			
VERSION	AI108811			
KEYWORDS	ALI08811.1 GI:5629115			
SOURCE	GSS.			
ORGANISM	Drosophila melanogaster (fruit fly)			
REFERENCE	Drosophila melanogaster			
AUTHORS	Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Peiryocta;			
TITLE	Neoptera; Endopterygota, Diptera; Brachycera; Muscomorpha;			
JOURNAL	Empyridae; Drosophilidae; Drosophila.			
COMMENT	1 (bases 1 to 1101)			
	Genoscope.			
	Direct Submission			
	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :			
	BP 191 91006 EVR cedex - FRANCE (E-mail : seqref@genoscope.cns.fr			
	- web : www.genoscope.cns.fr)			
	Determination of this BAC-end sequence was carried out as part of a			
	collaboration with the European Drosophila Genome Project (BDGP) -			
	http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC			
	library (Dros BAC) was made by Alain Billand at CEPH (Centre			

FEATURES		Location/Qualifiers	
source	1. 1101	/organism="Drosophila melanogaster"	
	/mol_type="genomic DNA"		
	/db_xref="taxon:7227"		
	/clone="BACN37D10"		
	/clone_1lb="DrosBAC"		
	/plasmid="pBelOBAC11"		
	/note="end : Sp6"		
ORIGIN			
Query Match	2.8%; Score 56.2; DB 10; Length 1101;		
Best Local Similarity	20.8%; Pred. No. 0.0093;		
Matches 123; Conservative 213; Mismatches 253; Indels 2; Gaps 1;			
Qy	421 GAGAGTTGGCTTACAGTAATCAATCCCTAAAAAATTGCTGACGTAAGTAAACATTC	480	
Db	507 GAGAAATGAGAGAGAAAAAAMAAAAAAMAAAAAMGKARGAAGRGRRBVGAR	566	
Qy	481 CAAGCAGCGGAAGAAGATTCACTAACTTTGACAGGTGCTATTATCAAGAGAAAGCT	540	
Db	567 GDATAATAAAAAADTCKRWDRGAAARAAAAADAAARAAKTTWAAAAAARAAAAA	626	
Qy	541 GAAATATTATTATTCCTACGTATGTGCAAGCTGCAAAATGCAATTTACTATTAAAG	600	
Db	627 AAAAAAAGATTTTAAAAAAGGGMGTGKGRKADGGAAADAWRRGRGRARAA	686	
Qy	601 GAGCGACTTAATATAAAAAAGATGGGACGTAGTGTCCACCGTTGATCCAGGTC	660	
Db	687 RAAAAADAKRAAAAAAAMAAAAAAMAAADGGRKMKKGDKGKATKTAAMWKGKRDW	746	
Qy	661 GGGAGAACTGATTGTAAACGCGGTTAAAAAGCGAAATATAAGTACTAATATTGT	720	
Db	747 GTATATWTTATATADTYKAAITTDKAAAGRRKRDRKRTARDDGRRATRRRMAAGK	806	
Qy	721 GTAAGGTGTATTAACAAGGTTTAGATCAGATAGAACAAGCGGTTCAAGTCTGAAGT	780	
Db	807 RARAGARAAAAARADRDMDMAAAAAAAMAAAAAAMTTWRDRWMDMDTRWDDTT	866	
Qy	781 TGTCCGAATTAATAAATTTCTGACAGAAATGACGTTGGCGGTATGATATTGCT	840	
Db	867 AAWWDADARARRRRRRRRRRARRRAADDTDKDWDADTTKDTTKTTTDDDD	926	
Qy	841 ATATTTCCACTATATGATTTGAAAAATATCCATATACACAAGGTGATGAGTTAAGT	899	
Db	927 WDAAKDRMAAARADGAKMRDRDRDWAATPAKDDDDWKMGGRGRRGGDKKRWGK	986	
Qy	900 -GGAAATTTATACAGCCAGTGGGATTCAGGGGAAATTAATGTTGGGAACGTTTT	958	
Db	987 TGKKDDDDMKWTRDRWMMWTTTKMDWMDWDGRRGRWTRKRGAWMRADAWARDJD	1046	
Qy	959 TTAGCTTAATTCGGTAGAAGCAATGAAACAGCGGACCTGTTAAGTTA 1009		
Db	1047 KDTFTADKDKRRTDTTKRDGDWKRKDKKRRDKDXTKKDATWDDDD 1097		
RESULT 3			
CNS000D1			
LOCUS			
DEFINITION	CNS000D1 1101 bp DNA linear GSS 03-JUN-1999		
ACCESSION	Drosophila melanogaster genome survey sequence T8T3 end of BAC #		
VERSION	BACR01J16 of RPL1-98 library from Drosophila melanogaster (fruit		
KEYWORDS	fly), genomic survey sequence.		
SOURCE	AL065414 GI:4938827		
ORGANISM	GSS.		
	Drosophila melanogaster (fruit fly)		
	Drosophila melanogaster		
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		

Db 931 TWKTTGTGTTTWMKGRNRGRGAGRRGRKKGAGKAGKMMKMAADABWTWTM 990

QY 1117 GGGCTTTTCAAGTATGCTGGAAGTAAATATCAGTAATATTTTGGC 1176

Db 991 DWMDWMKMTWDMGKRGWGDGRKGAADAKRRNRKRDGMRGNBAMKMDAAATKAR 1050

QY 1177 AATACCGATATATTAATTAATTTTCAAT 1205

Db 1051 WADDDWDADVDADADADYMKKATWMDW 1079

RESULT 5
CNS016B2/c
LOCUS
DEFINITION
1204 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN15A12 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL106628
AL106628.1 GI:5622852
GSS.
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1204)
Genoscope.
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billand at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES
Location/Qualifiers
source
1. 1204
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_1lb="BACN15A12"
/clone_1lb="DrosBAC"
/plasmid="pBelobAC11"
/note="end : T7"

ORIGIN
Query Match 2.6%; Score 51.8; DB 10; Length 1204;
Best Local Similarity 21.7%; Pred. No. 0.12; Indels 1; Gaps 1;
Matches 98; Conservative 16%; Mismatches 190;

QY 450 TAAAAAAGCTGCTGACGTAGTTAAAGCTCAAGCAGGGAAGAGATTCTAAACT 509

Db 1197 KAAWAAWATATWAKWAAWATATWAKWAKKAKWAKWAKWAKWAKWAKWAKWAKWAK 1138

QY 510 TTTAGCAGGCTCATTTCAAGACAGAAAGCTGAATATTTATTTGCTTACGATGTGCA 569

Db 1137 KKAIAAAAAAAAAAADAADAAAAAAAAAKAKAKAKAAAAAAAAAADAAMWKKMAAIAAK 1078

QY 570 AGCTGCAATGTGATTTATTTATTTAAGGACGCGTTAAATATATAA-AGAATGGG 628

Db 1077 WKATKDDDDKDAADAAKAKKAKKAKADKADKADKADKADKADKADKADKADKAKKAK 1018

QY 629 GACTAGTGTGCAACCGTTGATTCAGGTCAGGGAAGTGAAGTGAAGGCGTTAA 688

Db 1017 KXKKKDDATDADWAAWAAKAKKAKKAKKAKKAKKAKKAKKAKKAKKAKKAKKAKK 958

QY 689 AAGCGAAATTAAGATATCTAATATTTGTTAGGTTGATTAACAAGGTTTATATC 748

Db 957 KKAKKKKKAAKAAKAAAAAAAAKAKKAKKAKKAKKAKKAKKAKKAKKAKKAKKADAWADA 898

QY 749 AGATAAGACGGCGGTACAAAGTGTGAAGTTTGGTCAAAAATTATATAATTTGTAAG 808

Db 897 DPAAKKKAIAAKKKKKKDDADKADKADKADKADKADKADKADKADKADKADKADK 838

QY 809 AATGACGTTGGCGTATTTGATTTATTTGATTTATTTCAACTTATGATTTTGAATAAT 868

Db 837 AAKKKGKGGKGGGAGGAGGAAAGATTTWAKIDTTTKAKGDAKTTTTKTTTWTATGA 778

QY 869 ATTCATTAGCAACAAGTGTAGATTACTAG 899

Db 777 GAKWAKKTAADKADKADKADKADKADKADKADKADKADKADKADKADKADKADK 747

RESULT 6
CNS016D/c
LOCUS
DEFINITION
1225 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN15C18 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL106171
AL106171.1 GI:5620504
GSS.
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1225)
Genoscope.
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billand at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES
Location/Qualifiers
source
1. 1225
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_1lb="BACN15C18"
/clone_1lb="DrosBAC"
/plasmid="pBelobAC11"
/note="end : SP6"

ORIGIN
Query Match 2.5%; Score 51.4; DB 10; Length 1225;
Best Local Similarity 25.3%; Pred. No. 0.15; Indels 5; Gaps 1;
Matches 193; Conservative 158; Mismatches 406;

QY 4 AAAAAATGATTTCTTATCAAAATACAAATGAATGAATTCGATGCTCCCGAAT 63

Db 1190 WMAWMAAAAMWTTTATTAATAAATATATATATATATATATATATATATATATATW 1131

QY 64 AACACAAATATGTCAACAGATATCTTTGCAAGAGCAATATATATATCTCTTATAC 123

Db 1130 ATTWTATWATTAATAAATAATTTATTTAMWMAWMAWMAWMAWMAWMAWMAWMAWMA 1071

QY 124 CTGACGCTTGTGAGGAAAGCCATGCAAGATAGCTGGAATCAAGTCTCGATATAGTA 183

Db 1070 AAATATWATATATTAATAATWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMA 1011

QY 184 ACTATTGGACATACCTTATTAACAATTTCTGTAGAAACCGGATAGCTGGAATTCCTGTA 243

Db 1010 AAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMA 951

244 ATA-----TTTCATATAAACAACATTCCTCGCTGTCGTCATCTGTGACAC 298
 950 AATTTTATTTTATTTTATTTTAAATTTTATTTTATTTTATTTTATTTTATTTT 891
 299 TTTCTATATGATTTAGTATCTAATTTGTAAGAAGTACAGAGCGTGTAAAGT 358
 890 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 831
 359 ACCGGGTTGCAATTTTGAAGGTAATGACCTGTTTCAAGATTATTTATTTTATTC 418
 830 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 771
 419 TTGAGATGGCTTACAGATAATCAATCTTAAATAAATCTGCTGACGTATTTAAAGT 478
 770 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 711
 479 TCCAGACCGGAGAAAGATTTTCACTTAACTTTAGCAGGCTCTATTTCAAGACAGA 538
 710 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 651
 539 CTGAAATATTTATTTAGCTTACGTAATGCAAGCTGCAAAATGTCATTTTATTTAA 598
 650 AGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 591
 599 GGGACGAGTTAATTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 658
 590 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 531
 659 CAGGAGAACTGATTTGTAACGAGGCTTAAAGGAAATTAAGATTAATTAATTTAT 718
 530 NCTGNN 471
 719 GTGTAGGTTGTTAACAAGGTTTGTAGATCAGATTACAGACAGG 760
 470 AGTNN 429

RESULT 7
 CNS0102F/c 928 bp DNA linear GSS 26-JUL-1999
 LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC
 DEFINITION BACN03B09 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL098433 GI:5610044
 VERSION AL098433.1
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 928)
 Genoscope.
 Direct Submission
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (BDGP) -
 library (Dros BAC) was made by Alain Billard at CEPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelobAC11.
 FEATURES
 source 1..928
 Location/Qualifiers
 1..928
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACN03B09"
 /clone_lib="DrosBAC"
 /plasmid="pBelobAC11"

ORIGIN /note="end : T7"
 Query Match 2.5%; Score 50.6; DB 10; Length 928;
 Best Local Similarity 21.6%; Pred. No. 0.23;
 Matches 121; Conservative 172; Mismatches 268; Indels 0; Gaps 0;

344 AGACGCTTTAAGTGAACGGGTTGACAGATTGAGGTAATGACTGTTATCAAGATT 403
 922 AGACGGAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 863
 404 ATTATCTCATTTATCTGAGAGATTGGCTTACAGATAATCAATCTTAAAAAATCTG 463
 862 ATAKAKGTRGAKWTRADKDTGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 803
 464 ACCTAGTTAAACAGTTCCAGACGGAAGAAATTTCACTTAACTTTAGCAGGCTAT 523
 802 RAGKARMAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 743
 524 TATCAAGACGAAAGCTGAATATTTATTTATTTGCTTACGTAATGCAAGCTCAATGTC 583
 742 AATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 683
 584 ATTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 643
 682 TATDARARAKKWKATRAKAAAGATATRAAATGADAMGATWTGKTAAGKTGTAGWTG 623
 644 CGTTGATCCAGGCTGACGAGAACTGATTTGTAACGAGCGTTAAAGCGAAATAAAG 703
 622 RKTIDKRRRTDRTDRTDRTDRTDRTDRTDRTDRTDRTDRTDRTDRTDRTDRTD 563
 704 AGTATCTAATTTATTTGTAAGGTTGTAACAAGGTTTGTAGATCAGATTACAGACAG 763
 562 TRKAGAADRRAGAAAAAGTGTADADKRAAGKXGDKDKRTGTGRTATGGRAGRA 503
 764 GTCAAGTGTGAAGTTTGTGCAAAATTTATTTATTTGCTAGAGAAATACGTTGGCG 823
 502 KDDKRRGKWKRRKAKDKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTK 443
 824 TATTGATATTTATTTGCTATTTTCAACTATGATTTTGAATTTTCACTTAAAGCA 883
 442 ATATRTGKMGWMDWATTGATTTATTTATTTATTTATTTATTTATTTATTTATTT 383
 884 GTGTAGATTTACTAGGAAA 904
 382 AAKGAGAAKAGRAAARAAA 362

RESULT 8
 CNS00ES1/c 1101 bp DNA linear GSS 04-JUN-1999
 LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC:
 DEFINITION BACR2915 of RCLT-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL069797 GI:4949738
 VERSION AL069797
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1101)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Oosogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPci-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

1. 1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR29L15"
/clone_lib="RPci-98"
/note="end : TET3"

ORIGIN

Query Match 2.5%; Score 49.6; DB 10; Length 1101;
Best Local Similarity 21.0%; Pred. No. 0.42;

Matches 112; Conservative 171; Mismatches 250; Indels 0; Gaps 0;

FEATURES

source

1. 938
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14U11"
/clone_lib="RPci-98"
/note="end : T7"

ORIGIN

Query Match 2.4%; Score 48.4; DB 10; Length 938;
Best Local Similarity 21.8%; Pred. No. 0.82;

Matches 84; Conservative 152; Mismatches 148; Indels 2; Gaps 1;

FEATURES

source

1. 938
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14U11"
/clone_lib="RPci-98"
/note="end : T7"

ORIGIN

Query Match 2.4%; Score 48.4; DB 10; Length 938;
Best Local Similarity 21.8%; Pred. No. 0.82;

Matches 84; Conservative 152; Mismatches 148; Indels 2; Gaps 1;

FEATURES

source

1. 938
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14U11"
/clone_lib="RPci-98"
/note="end : T7"

ORIGIN

Query Match 2.4%; Score 48.4; DB 10; Length 938;
Best Local Similarity 21.8%; Pred. No. 0.82;

Matches 84; Conservative 152; Mismatches 148; Indels 2; Gaps 1;

FEATURES

source

1. 938
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14U11"
/clone_lib="RPci-98"
/note="end : T7"

ORIGIN

Query Match 2.4%; Score 48.4; DB 10; Length 938;
Best Local Similarity 21.8%; Pred. No. 0.82;

Matches 84; Conservative 152; Mismatches 148; Indels 2; Gaps 1;

REFERENCE

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.

AUTHORS

1 (bases 1 to 938)

TITLE

Journal

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oosogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPci-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

1. 938
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14U11"
/clone_lib="RPci-98"
/note="end : T7"

ORIGIN

Query Match 2.4%; Score 48.4; DB 10; Length 938;
Best Local Similarity 21.8%; Pred. No. 0.82;

Matches 84; Conservative 152; Mismatches 148; Indels 2; Gaps 1;

FEATURES

source

1. 938
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14U11"
/clone_lib="RPci-98"
/note="end : T7"

ORIGIN

Query Match 2.4%; Score 48.4; DB 10; Length 938;
Best Local Similarity 21.8%; Pred. No. 0.82;

Matches 84; Conservative 152; Mismatches 148; Indels 2; Gaps 1;

FEATURES

source

1. 938
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14U11"
/clone_lib="RPci-98"
/note="end : T7"

ORIGIN

Query Match 2.4%; Score 48.4; DB 10; Length 938;
Best Local Similarity 21.8%; Pred. No. 0.82;

Matches 84; Conservative 152; Mismatches 148; Indels 2; Gaps 1;

FEATURES

source

1. 938
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14U11"
/clone_lib="RPci-98"
/note="end : T7"

ORIGIN

Query Match 2.4%; Score 48.4; DB 10; Length 938;
Best Local Similarity 21.8%; Pred. No. 0.82;

Matches 84; Conservative 152; Mismatches 148; Indels 2; Gaps 1;

RESULT 9
CNS006TJ/c 938 bp DNA linear GSS 03-JUN-1999
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14U11 of RPci-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AL065906
GI:4944874
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

RESULT 10
CNS0106X 1101 bp DNA linear GSS 26-UTL-1999
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN03K20 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

AL098595

KEYWORDS	AL098595.1	GI:5610206
SOURCE	GSS.	
ORGANISM	Drosophila melanogaster (fruit fly)	
REFERENCE	Drosophila melanogaster	
AUTHORS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyridiidae; Drosophilidae; Drosophila.	
TITLE	1 (bases 1 to 1101)	
JOURNAL	Genoscope.	
COMMENT	Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqef@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk/. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billard at CEPH (Centre d'etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.	
FEATURES	Location/Qualifiers	
source	1..1101 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /db_xref="taxon:7227" /clone="BACN03K20" /clone_11b="DrosBAC" /plasmid="pBeloBAC11" /note="end : 17"	
ORIGIN		
Query Match	2.4%; Score 48.2; DB 10; Length 1101;	
Best Local Similarity	19.1%; Pred. No. 0.95;	
Matches	107; Conservative 227; Mismatches 220; Indels 7; Gaps 2;	
QY	361 GGGGTTCAGAGTTTGGAGCGTGAATGACTGCTTATCAAGATTATTAATCTTATCTT 420	
DB	547 GKGCTCGAGRGRTGCVKKEKHTHTHTTGKHKHTCTCHKHTTWTMTTWAKAKGTG 606	
QY	421 GAGGATTCGCTTACGATTAATCAATCCTTAATAAACTTGCAGCTGATTAACAGTTC 480	
DB	607 TGTDDKATKATMATGATGATATRTTAAATKTAATKTAATDTRTAATATATKATKKARXKD 666	
QY	481 CAAGCAGCGGAAGAATCTTACTTAACTTTAGCAGCGTCAATTAACAAGAGTTC 540	
DB	667 TAAKAMKMDKATPKAKAKKAKKAKKAAKATATGDAKAKAKAKAKATKAKAKAAWTA 726	
QY	541 GAAATATTATTATTGCTTACGATGTCGACGCTCAAAATGTGCATTATTATCTATTAAAG 600	
DB	727 TWTATTAADAAADK---GAKDKAKAKAKAADARDKRRWDAKDKKRAKAKAAKADADA 782	
QY	601 GAGCAGTTAAATATNAAAAAAGATGGGGAAGTCAAGTGTCCACCGTGTATCCAGGTC 660	
DB	783 DAKAKAADAAKAKAADADDERGGGKKKRAADRRKKKKKDKRAWDDKKKAK--KDXAA 839	
QY	661 GGAAGAATCGATTGTAACGACGGTTTAAAGGAAATTAAGAGTATTAATTAATTGT 720	
DB	840 KAKADADADAKAKRRRABDKAKADAAAKAKAKAKDDDAKATKAKATKAKKDKAKA 899	
QY	721 GTAGGCTGTATTAACAAGGTTTATGATCAGATTAAAGCAGCGGCTACAAGTCTGAAGTT 780	
DB	900 KKKKKKKDKDAKAKAKAKADKDKDKDKDKDKDKAKDKKKKKKDKRADKAKKDDDKDK 959	
QY	781 TGTGTGAATTTAATTAATTTTCGTAGAGAAATGACGTGGCGGTATTGGATTTATTGCT 840	
DB	960 KAKDKDKDKDADAAKAAKADADAKAKAKAKAAADDDAAADKAAADAKAKAKAKA 1019	
QY	841 ATATTCCAACTTATGATTTGAAAAAATATCATTAAGCAACAGTGTAGATTAATAG 900	
DB	1020 DDAKAKAKKADAKAADADAKAKAAKRAKATADADAATAKAKKADKDKDAKKDDAKKK 1079	
QY	901 GAAATTTATACAGATCCAGTG 921	

DB	1080	AKADAAKAKAKAKAKKD	1100
RESULT 11			
CNS00LOO/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
SOURCE			
ORIGIN			

OY		966	TAAATTCGGTAGAAGCAATGGAACCGGGAACCTGTATTAGTACTTGCCCTCAAGCAT	1025
Dd		597	KADDTGGKGAARGGKRGKRKYDKAKGADKGATGAAKKGTAKKGDHAKKKDGRADGD	538
OY		1026	AGATAATATATAGTCAATTTCTTAATTCCTCAGCTTGTTACTTAAATGAGCTGGGAGGGAAC	1085
Dd		537	ARTRGGKAKKKKTKKGTKKDKKGGTDKKGATRTGTEBRGAGAGDGADGOTGTGTGKGAR	478
OY		1086	TCGCATTTATGAAGACTTCACAAAAGGCTAACCGTGCTTTTCAACGTATGTCTGGA	1140
Dd		477	GKGAAGAAGVAAARFAGAGGAGAKRGGTGTTRGKKAGAGGWGGRKDAAGWKAKGR	423
RESULT 12				
LOCUS	CNS075BG/c			
DEFINITION	CNS075BG	867 bp	DNA	linear
ACCESSION	clone BA0AB034D05 of library BA0AB from strain CLIB 210 of			
VERSION	Kluyveromyces lactis, genomic survey sequence.			
KEYWORDS	AL429890			
SOURCE	Al429890.1 GI:12213084			
ORGANISM	GSS.			
REFERENCE	Kluyveromyces lactis			
AUTHORS	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Kluyveromyces lactis			
REFERENCE	Saccharomycetales: Saccharomycetaceae: Kluyveromyces.			
AUTHORS	1 (bases 1 to 867)			
TITLE	Soucieur,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bojotin-Pikuhara,M., Bon,E., Brotlier,P., Casaregola,S., de-Montigny,U., Dujon,B., Durieux,P., Lepingle,A., Lorente,B., Malpertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekra,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.			
JOURNAL	Genomic exploration of the hemiascomycetous yeasts : 1. A set of yeast species for molecular evolution studies			
PUBMED	FEMS Lett. 487 (1), 3-12 (2000)			
REFERENCE	1152876			
AUTHORS	2 (bases 1 to 867)			
TITLE	Bojotin-Pikuhara,M., Toffano-Nioche,C., Artiguenave,F., Duchateau-Nguyen,G., Lemaitre,M., Marnelise,R., Montrocher,R., Robert,C., Termelier,M., Wincker,P. and Wesolowski-Louvel,M.			
JOURNAL	Genomic exploration of the hemiascomycetous yeasts : 11. Kluyveromyces lactis			
PUBMED	FEMS Lett. 487 (1), 66-70 (2000)			
REFERENCE	1152886			
AUTHORS	3 (bases 1 to 867)			
TITLE	Genoscope.			
JOURNAL	Direct Submission			
PUBMED	Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,			
REFERENCE	2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : begref@genoscope.cns.fr - Web : www.genoscope.cns.fr)			
AUTHORS	This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sobditophylla, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.			
COMMENT	Location/Qualifiers			
FEATURES	1..867			
SOURCE	/organism="Kluyveromyces lactis"			
	/mol_type="genomic DNA"			
	/strain="CLIB 210"			
	/variety="lactis"			
	/db_xref="taxon:28985"			
	/clone="BA0AB034D05"			
	/clone_1fb="BA0AB"			
ORIGIN				
Query Match	2.3%	Score 46.6;	DB 11;	Length 867;
Best Local Similarity	39.7%;	Pred No. 2.3;		

[illegible]

/clone="HRC12957"
/tissue_type="kidney"
/cell_type="epithelial cell"
/clone_lib="Sugano cDNA library, kidney epithelial cell"

ORIGIN

Query Match 2.3%; Score 46.4; DB 3; Length 572;
Best Local Similarity 49.6%; Pred. No. 2.3;
Matches 119; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 386 TGACCTGTTTCAAGATTATTTATCTTATCTTGAAGATTGGCTTACAGATTAATCA 445
DB 8 TTATGCTTATGCGAAGCTCAGATCTGTTGCTTTGGAGAACTGAGAACAAAGAA 67
QY 446 ATCTTAAAAAATTGCTGACGTTAAACAGTTTCAAGACGGGAGAAAGATTCTACTA 505
DB 68 TTATATAGTACTAGATGAAATAGTGAAGAGTGAAGCCAAAGCCAAATTTTGAAC 127
QY 506 AACTTTTACAGAGGCTCTTTTCAAGACAGAAAGCTGAAATTTTATTGCTTACGATG 565
DB 128 GCCAGCGCTGAGAAATATGAACTGACAGAAAGCTGAGCAAGTTTATGTTTAAAGCTG 187
QY 566 TGCAGCTGCAAAATGTCATTTTATCTATTAAGGACGAGTTAATATTAATAAAGAT 625
DB 188 AACAGCTATGAGAGAGATTGACGATTGACAGAGACACTGATTAAGCCAAACAGCAAT 247

RESULT 14
AA448366 355 bp mRNA linear EST 04-JUN-1997
LOCUS z996c06.r1 Soares_total_fetus_Nb2H8_9w Homo sapiens cDNA clone
DEFINITION IMAGE:784810 5' similar to gb:X66397_cds1 TPR ONCOGENE (HUMAN);
mRNA sequence.

ACCESSION AA448366
VERSION AA448366
KEYWORDS EST. 2162036
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 355)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Scheinberg, K., Stepcoe, M., Tan, F., Theising, B.,
White, Y., Wyllie, T., Waterston, R. and Wilson, R.
Washu-Merck EST Project 1997
COMMENT Unpublished (1997)

TITLE
JOURNAL
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu

FEATURES
source
1. 355
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5982428"
/db_xref="taxon:9606"
/clone="IMAGE:784810"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/clone_lib="Soares_total_fetus_Nb2H8_9w"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAATCGAAGGAGGAGGCGCGTTATTTTATTTTATTTT 3']
Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 2.3%; Score 46; DB 1; Length 355;
Best Local Similarity 49.6%; Pred. No. 2.6;
Matches 118; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 388 ACTGCTTATCAATATTTATTTCTTATCTTGAAGATTGGCTTACAGATTAATCAAT 447
DB 23 AATGCTTATGCGAAGCTCAGATCTGTTGCTTTGGAGAACTGAGAACAAAGAAAT 82
QY 448 CTTAAAAAATTGCTGACGTTAAACAGTTTCAAGACGGGAGAAAGATTCTACTAA 507
DB 83 AATTAAGTACTAGATGAAATATGAAAGAGTGAAGCCAAAGCCAAATTTTGAACG 142
QY 508 CTTTACAGAGGCTCTTTTCAAGACAGAAAGCTGAAATTTTATTGCTTACGATG 567
DB 143 CACCGTGAAGAAATATGAACTGACAGAAAGCTGAGCAAGTTTATCTGTTAAGCTTGA 202
QY 568 CAGCTGCAAAATGTCATTTTATCTATTAAGGACGAGTTAATATTAATAAAGAT 625
DB 203 CAAGCTATGAGAGATTGACGATTGACAGAGACACTGATTAAGCCAAACAGCAAT 260

RESULT 15
CB158772 511 bp mRNA linear EST 29-JAN-2003
LOCUS K-EST0218180 l18POOLn1 Homo sapiens cDNA clone l18POOLn1-14-D04
DEFINITION 5', mRNA sequence.

ACCESSION CB158772
VERSION CB158772
KEYWORDS EST. 28143910
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 511)
AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
COMMENT Unpublished (2002)

TITLE
JOURNAL
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boseon-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.krdb.re.kr
Plate: 14 row: D column: 04
High quality sequence stop: 511.
Location/Qualifiers

FEATURES

source
1. 511
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="l18POOLn1-14-D04"
/cell_line="SNU-354+Cho-CK+Cho-CK+HLK-3"
/lab_host="Top10F"
/clone_lib="l18POOLn1"
/note="Organ: Liver; Vector: pT73-Pac; Site 1: EcoRI;
Site 2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."

ORIGIN

Query Match 2.3%; Score 46; DB 6; Length 511;

Best Local Similarity 49.6%; Pred. No. 2.8; Mismatches 120; Indels 0; Gaps 0;
 Matches 118; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
 QY 388 ACTGCTTATCAAGATTATATCTTCATTACTTGAGGATTGCTTACAGATAATCAAA 447
 Db 186 AATGCTTATGTGAACTCAGATCAGTTGCTTTGGAGAACTAGAGAACAAAGATT 245
 QY 448 CTTAAAAAAGCTTCTGACGTAGTTAAACAGTCCAAAGCAGGGAAGATTTCACCTAAA 507
 Db 246 AATTAAGTACCTAGATGAAATAGTAAAGAGTGAAGCCAAAGCACCMAATTTGAAACGC 305
 QY 508 CTTTTCAGAGGTCATTATCAAGACAGAAAGCTGAATATTTATTGCTTACGTATGTG 567
 Db 306 CAGCGTGAGGAATATGACGTGCAAGAAAGCTGTAGCAAGTTATCTGTAAAGCTTGAA 365
 QY 568 CAAAGTGCAAATGTGATTATTAATTAAGGAGCAGTTAATATATAAAAAAGAT 625
 Db 366 CAAGCTATGAAAGAGATTGACGATTGACAGAGAGACATGATTAAGCAACCAAGCAAT 423

Search completed: December 19, 2005, 12:54:29
 Job time : 5410.27 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 02:23:18 ; Search time 810.703 Seconds

(without alignments)
16597.955 Million cell updates/sec

Title: US-10-782-141-2

Sequence: 1 gtgtataaatgatactctta.....atagttattcatcaattaa 2019

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_21.*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2019	100.0	2019	13	Adt89414 AXMI-008
2	2019	100.0	2145	13	Adt89413 AXMI-008
3	2010	99.6	2010	13	Adt89416 AXMI-008
4	747.2	37.0	2082	13	Adt89401 AXMI-008
5	747.2	37.0	5980	13	Adt89400 AXMI-008
6	739.8	36.6	2073	13	Adt89403 AXMI-008
7	174	8.6	1983	3	Aaz93234 Sequence
8	174	8.6	3837	3	Aaz93235 Sequence
9	172.4	8.5	3471	2	Aax16515 DNA encod
10	172.4	8.5	3471	2	Aax16515 Bacillus
11	162.8	8.1	2407	4	Aas02478 B. thurin
12	133.6	6.6	4391	14	Aae61394 Bacillus
13	119.8	5.9	1959	4	Aas02466 B. thurin
14	118.4	5.9	1986	3	Adt89411 AXMI-009
15	118.4	5.9	2016	13	Adt89409 AXMI-009
16	118.4	5.9	2049	13	Adt89407 AXMI-009
17	118.2	5.9	3687	12	Adt88478 B. thurin
18	118.2	5.9	3932	2	Aag64112 CRYETS ge
19	118.2	5.9	3932	2	Aaz09160 B. thurin

20	118.2	5.9	3934	2	AAT95051
21	118.2	5.9	3934	2	AAT68434
22	118.2	5.9	3934	2	AAV83927
23	117.6	5.8	1806	13	Adt89392
24	117.6	5.8	1890	13	Adt89390
25	117.6	5.8	2190	13	Adt89389
26	116.8	5.8	3684	2	AAV15222
27	116.8	5.8	3684	4	AAAB9221
28	116.8	5.8	3684	4	AAAB9221
29	113.4	5.6	2019	8	ABV93759
30	112.4	5.6	3687	4	AAH8240
31	112.4	5.6	4173	4	AAAB2482
32	111.8	5.5	1897	2	AAV13118
33	111.8	5.5	1897	3	AAZ39905
34	111.8	5.5	1897	4	AAH26983
35	111.8	5.5	2019	8	ABV93756
36	111.8	5.5	2019	8	ABV93757
37	111.8	5.5	3471	2	AAV16516
38	111.8	5.5	3471	2	AAH83877
39	111.8	5.5	3471	4	AAAB2477
40	111.8	5.5	3471	4	AAH19323
41	111.8	5.5	4344	2	AAAB6782
42	111.8	5.5	4344	2	AAAB6782
43	110.2	5.5	2019	8	ABV93758
44	107.8	5.3	2160	4	AAAB4855
45	107.8	5.3	2965	2	AAAB6636

ALIGNMENTS

RESULT 1	
ID	Adt89414 standard; cDNA; 2019 BP.
XX	
AC	Adt89414;
XX	
DT	18-NOV-2004 (first entry)
XX	
DE	AXMI-008 coding sequence.
XX	
KW	ser; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW	expression cassette; transformation; transgenic; plant; bacteria;
KW	lepidoptera; coleoptera; pest; pesticide; resistance;
KW	pesticidal activity.
XX	
OS	Bacillus thuringiensis.
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	1..2019
FT	/*tag= a
FT	/tranyl_except= pos:1..3, aa:Met
XX	
XX	WO2004074462-A2.
XX	
PD	02-SEP-2004.
XX	
PF	20-FEB-2004; 2004WO-US05829.
XX	
XX	20-FEB-2003; 2003US-0448632P.
PR	20-FEB-2003; 2003US-0448633P.
PR	20-FEB-2003; 2003US-0448797P.
PR	20-FEB-2003; 2003US-0448806P.
PR	20-FEB-2003; 2003US-0448810P.
PR	20-FEB-2003; 2003US-0448812P.
PR	19-FEB-2004; 2004US-00781979.
PR	19-FEB-2004; 2004US-00782020.
PR	19-FEB-2004; 2004US-00782096.
PR	19-FEB-2004; 2004US-00782141.
PR	19-FEB-2004; 2004US-00782570.
PR	19-FEB-2004; 2004US-00783417.
XX	
XX	Aat95051 DNA encod
XX	Aat68434 CRYETS ge
XX	AAV83927 DNA encod
XX	Adt89392 AXMI-004
XX	Adt89390 AXMI-004
XX	Adt89389 AXMI-004
XX	AAV15222 Bacillus
XX	AAAB9221 Bacillus
XX	AAAB9221 B. thurin
XX	ABV93759 B. thurin
XX	AAH8240 Nucleotid
XX	AAS02482 B. thurin
XX	AAV13118 Bacillus
XX	AAZ39905 Truncated
XX	Aah26983 Coding se
XX	ABV93756 Bacillus
XX	ABV93757 B. thurin
XX	AAV16516 DNA encod
XX	AAH83877 Bacillus
XX	AAAB2477 B. thurin
XX	Aah19323 CRYC cod
XX	AAAB6782 Insectici
XX	AAAB6782 Insectici
XX	ABV93758 B. thurin
XX	ABV93758 B. thurin
XX	AAAB4855 Bacillus
XX	Aag6636 Gene enco

PA (ATHE-) ATHENIX CORP.
XX Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;
XX MPI, 2004-635574/61.
XX P-PSDB; ADR89415.
XX
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
XX PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
XX PT for producing organisms with pesticide resistance.
XX
XX Claim 1; SEQ ID NO 26; 178bp; English.
XX
XX This sequence encodes an isolated delta-endotoxin. Some of the delta-
XX endotoxin coding sequences of the invention have alternative start frame.
XX The nucleic acid sequences of the invention are useful in DNA constructs
XX or expression cassettes for transformation and expression in plants and
XX bacteria. The nucleic acids and corresponding polypeptides are useful for
XX killing lepidopteran or coleopteran pests. Compositions containing the
XX delta-endotoxins of the invention, and methods for their production, are
XX useful for the production of organisms with pesticide resistance,
XX specifically bacteria and plants. These organisms are useful for
XX generating altered or improved delta-endotoxin or delta-endotoxin-
XX associated proteins that have pesticidal activity, or for detecting the
XX presence of delta-endotoxin or delta-endotoxin-associated proteins or
XX nucleic acids in products or organisms.
XX
XX Sequence 2019 BP; 662 A; 324 C; 419 G; 614 T; 0 U; 0 Other;

Query Match 100.0%; Score 2019; DB 13; Length 2019;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGAAAATATGATCTTATTCAAAATCAATGATGAAATTCGATGTTCCCG 60
DB 1 GTGAAAATATGATCTTATTCAAAATCAATGATGAAATTCGATGTTCCCG 60
QY 61 AATAACAAATATGTCAAACAGATATCTTTGCAAGGATCCAAATATTTCTATT 120
DB 61 AATAACAAATATGTCAAACAGATATCTTTGCAAGGATCCAAATATTTCTATT 120
QY 121 AACCTGACGCTTGTGACGGAGAGCCATGACAGATACGTGGAAATCAGTCGATATA 180
DB 121 AACCTGACGCTTGTGACGGAGAGCCATGACAGATACGTGGAAATCAGTCGATATA 180
QY 181 GTACTATTTGGGACATACCTTATTAACAATTTCTGTAGAACCGGATATAGGTGAATTCCT 240
DB 181 GTACTATTTGGGACATACCTTATTAACAATTTCTGTAGAACCGGATATAGGTGAATTCCT 240
QY 241 GTAATATTTTCAATTAATAACAACATCCTCGCTTCTGTGCAATCTGTGGACAGACTT 300
DB 241 GTAATATTTTCAATTAATAACAACATCCTCGCTTCTGTGCAATCTGTGGACAGACTT 300
QY 301 TCTATATGTGATTTAGTATCTAATATTCGTAAAGAGTAGACGAGCGGTAAAGTAGAC 360
DB 301 TCTATATGTGATTTAGTATCTAATATTCGTAAAGAGTAGACGAGCGGTAAAGTAGAC 360
QY 361 GGGGGTTCAGATTTTGAAGGTGAATGACTGCTTATCAAGATTAATATTTCTTCAATTCCT 420
DB 361 GGGGGTTCAGATTTTGAAGGTGAATGACTGCTTATCAAGATTAATATTTCTTCAATTCCT 420
QY 421 GAGGATTTGGCTTACAGATAATCAATCCTTAAACCTTGCAAGTAAACAGTTTC 480
DB 421 GAGGATTTGGCTTACAGATAATCAATCCTTAAACCTTGCAAGTAAACAGTTTC 480
QY 481 CAAGCAGGAGAGAGATTTCACTAAACCTTTAGCAGGGTCATTATCAAGACAGAAAGCT 540
DB 481 CAAGCAGGAGAGAGATTTCACTAAACCTTTAGCAGGGTCATTATCAAGACAGAAAGCT 540
QY 541 GAAATATTTATTTAGCTACGATATGTCAGAGCTGCAAAATGCAATTAATTAATTAAGG 600
DB 541 GAAATATTTATTTAGCTACGATATGTCAGAGCTGCAAAATGCAATTAATTAATTAAGG 600

QY 601 GACGAGTTAATATATTAATAAAGATGGGACCTAGTGTCCACCGTTGATCCAGGATCA 660
DB 601 GACGAGTTAATATATTAATAAAGATGGGACCTAGTGTCCACCGTTGATCCAGGATCA 660
QY 661 GGGAGACTGATTTGTATACGAGCGGTTAAAGGGAATTAAGAGATATCTAATTAATGT 720
DB 661 GGGAGACTGATTTGTATACGAGCGGTTAAAGGGAATTAAGAGATATCTAATTAATGT 720
QY 721 GTAGGGGTGATTAACAAGGGTTTAAATCATCAATCAAGCGGGTCAAGTCTGAAGTT 780
DB 721 GTAGGGGTGATTAACAAGGGTTTAAATCATCAATCAAGCGGGTCAAGTCTGAAGTT 780
QY 781 TGGTGAAATTTAATAAATTTTGTAGAGAAATGAGCTTGGCTTGAATTTATTTGCT 840
DB 781 TGGTGAAATTTAATAAATTTTGTAGAGAAATGAGCTTGGCTTGAATTTATTTGCT 840
QY 841 AATATTTCCAACTTATGATTTGAAAAATATCCATTAGCAACAAGTATAGTTAACTAG 900
DB 841 AATATTTCCAACTTATGATTTGAAAAATATCCATTAGCAACAAGTATAGTTAACTAG 900
QY 901 GAAATTTATACATTCAGTCCAGTGGGATATTCAGGGGAAATTAATGTTGGAAACGTTT 960
DB 901 GAAATTTATACATTCAGTCCAGTGGGATATTCAGGGGAAATTAATGTTGGAAACGTTT 960
QY 961 AGCTTTAATTTGGTGAAGCAAAATGGAACAAGGGGACCTGGTTTATGTTACTTGGCTCA 1020
DB 961 AGCTTTAATTTGGTGAAGCAAAATGGAACAAGGGGACCTGGTTTATGTTACTTGGCTCA 1020
QY 1021 GCTATAGATATATATATGATCATCTATTAATCTTCAGCTTGGTATATAGTGGTGGGG 1080
DB 1021 GCTATAGATATATATATGATCATCTATTAATCTTCAGCTTGGTATATAGTGGTGGGG 1080
QY 1081 GGAATCTGTCATTAATGAGACATTCACAAAGGTAACGGTCTTTCAACGATATGCTGGA 1140
DB 1081 GGAATCTGTCATTAATGAGACATTCACAAAGGTAACGGTCTTTCAACGATATGCTGGA 1140
QY 1141 ACTAGAGATTAATATCCAGTAAATTTATTTTGGCAATACCGATATATTTAAATTTAT 1200
DB 1141 ACTAGAGATTAATATCCAGTAAATTTATTTTGGCAATACCGATATATTTAAATTTAT 1200
QY 1201 TCATTAGCTAGATATGACATGCAACCGTTTGTGGGATTCATATCCACGGCATCTGTT 1260
DB 1201 TCATTAGCTAGATATGACATGCAACCGTTTGTGGGATTCATATCCACGGCATCTGTT 1260
QY 1261 TCAAGTGCAGAAATTTTTCGACAAACATTAATCTTCTGTATGAGGTAACAGTTCT 1320
DB 1261 TCAAGTGCAGAAATTTTTCGACAAACATTAATCTTCTGTATGAGGTAACAGTTCT 1320
QY 1321 GGGTACTCACAACAATGGAATCTGTGTTACAGAGTAATTAAGGATCTACACCTAGT 1380
DB 1321 GGGTACTCACAACAATGGAATCTGTGTTACAGAGTAATTAAGGATCTACACCTAGT 1380
QY 1381 CGTACAAATTAATCTCATAGATTAATCAATGCGGATGTTCAAATGAAACCTCCAGA 1440
DB 1381 CGTACAAATTAATCTCATAGATTAATCAATGCGGATGTTCAAATGAAACCTCCAGA 1440
QY 1441 GTTAAAGTATTTGTTGGACACATACAGTAAAGGAAATTAATGCAATTTATCCAGAT 1500
DB 1441 GTTAAAGTATTTGTTGGACACATACAGTAAAGGAAATTAATGCAATTTATCCAGAT 1500
QY 1501 AAAATTTAGCAAAATTCGCACTAAAGCTTTTCCCTACAGCAGAGTACAGGATATGGA 1560
DB 1501 AAAATTTAGCAAAATTCGCACTAAAGCTTTTCCCTACAGCAGAGTACAGGATATGGA 1560
QY 1561 GAGAGTTACGTACAGCTGGGCTGGTTTATACAGAGAGAGTATGTAACGTTACCTTAT 1620
DB 1561 GAGAGTTACGTACAGCTGGGCTGGTTTATACAGAGAGAGTATGTAACGTTACCTTAT 1620
QY 1621 CAAGCAAGTTTAAATAATACGTTTAACTTGTGACCCACGAATTAATTAATTAATTAAT 1680
DB 1621 CAAGCAAGTTTAAATAATACGTTTAACTTGTGACCCACGAATTAATTAATTAATTAAT 1680

PT	New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
FT	and polypeptides, useful for killing lepidopteran or coleopterian pests or
LT	for producing organisms with pesticide resistance.
XX	
PS	Claim 1; SEQ ID NO 25; 178bp; English.
XX	
CC	This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC	endotoxin coding sequences of the invention have alternative start
CC	codons, producing more than one protein from a single open reading frame.
CC	The nucleic acid sequences of the invention are useful in DNA constructs
CC	or expression cassettes for transformation and expression in plants and
CC	bacteria. The nucleic acids and corresponding polypeptides are useful for
CC	killing lepidopteran or coleopterian pests. Compositions containing the
CC	delta-endotoxins of the invention, and methods for their production, are
CC	useful for the production of organisms with pesticide resistance,
CC	specifically bacteria and plants. These organisms are useful for
CC	generating altered or improved delta-endotoxin or delta-endotoxin-
CC	associated proteins that have pesticidal activity, or for detecting the
CC	presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC	nucleic acids in products or organisms.
XX	
CC	
SQ	Sequence 2145 BP; 710 A; 338 C; 441 G; 656 T; 0 U; 0 Other;
Query Match	100.0%; Score 2019; DB 13; Length 2145;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 2019; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GTGAAAAATATGAATCTTATCAAAATAACAAATGATGAAATTCGGATGTCCCGC 60
DB	127 GTGAAAATATGAATTCTTATCAAATAACAATGAAATGAAATTCGGATGTCCCGC 186
OY	61 AATAACACAATATATGTCAAAACAGATATCTTTTGCAAAAGATCCAATATATTTCTATT 120
DB	187 AATAACACAATATATGTCAAAACAGATATCTTTTGCAAAAGATCCAATATATTTCTATT 246
OY	121 AACCTGCACGCTTGTCAAGGAGGCCAATGCGACAGATACGTGGAAATCATGCTCGATATA 180
DB	247 AACCTGCACGCTTGTCAAGGAGGCCAATGCGACAGATACGTGGAAATCATGCTCGATATA 306
OY	181 GTAACCTATTTGGGAATACCTTATCATATCTTGTGTAAACCCTGTAATAGTGGAAATTCCT 240
DB	307 GTAACCTATTTGGGAATACCTTATCATATCTTGTGTAAACCCTGTAATAGTGGAAATTCCT 366
OY	241 GTAATATTTTCAATAATAAACAAACTGATCCGCTCTGCGTCAATCTGTGGACGACTT 300
DB	367 GTAATATTTTCAATAATAAACAAACTGATCCGCTCTGCGTCAATCTGTGGACGACTT 426
OY	301 TCATATATGTGATTTAGTATCTATATATTCGTAAAGAGGTAGAAGAGCGTGTAAAGTGAC 360
DB	427 TCATATATGTGATTTAGTATCTATATATTCGTAAAGAGGTAGAAGAGCGTGTAAAGTGAC 486
OY	361 GGGGTTCAGATTTTGGAGGTGAAATGACGTCTTATCAAGATTATATCTTCATTATCTT 420
DB	487 GGGGTTCAGATTTTGGAGGTGAAATGACGTCTTATCAAGATTATATCTTCATTATCTT 546
OY	421 GAGGATTTGGCTTACAGATTAATCAAAATCCPAAAAAACTTGCTGACGTAGTTAAACAGTTC 480
DB	547 GAGGATTTGGCTTACAGATTAATCAAAATCCPAAAAAACTTGCTGACGTAGTTAAACAGTTC 606
OY	481 CAAGCACGGGAGAGATTTCACTTAACTTTTAGCAGGGTCATATATCAAGACAGAAAGCT 540
DB	607 CAAGCACGGGAGAGATTTCACTTAACTTTTAGCAGGGTCATATATCAAGACAGAAAGCT 666
OY	541 GAAATATTTATTTATTCCTACGTATGTGCAAGCTGCAAAATGTGCATTTATTAATTAAG 600
DB	667 GAAATATTTATTTATTCCTACGTATGTGCAAGCTGCAAAATGTGCATTTATTAATTAAG 726
OY	601 GAGCAGATTTAAATATTAATAAAAGAAATGGGAGCTAGTGTGCCACCGTGTATCCAGGGGTCA 660
DB	727 GAGCAGATTTAAATATTAATAAAAGAAATGGGAGCTAGTGTGCCACCGTGTATCCAGGGGTCA 786
OY	661 GGAGGAACTGATTTGTAACGACGGCTTAAAAACGAAAAATAAAGATATTAATTAATTTGT 720

Db 787 GGGAGAACGATTGTATACGAGCGGTTAAAGCGAAATTAAGATATCTATTATGT 846
Qy 721 GTTAGGTGTATATACAAAGGTTTATGATCAGATTAAGACGGCGGTTCAAGTCTGAAGTT 780
Db 847 GTAGGGTGTATTAACAAGGTTTATGATCAGATTAAGACGGCGGTTCAAGTCTGAAGTT 906
Qy 781 TGGTCAAAATTTAATAATTTGTAGAGAAATGACGTGGCGGTTATTTGATATATTTGCT 840
Db 907 TGGTCAAAATTTAATAATTTGTAGAGAAATGACGTGGCGGTTATTTGATATTTGCT 966
Qy 841 ATATTTTCCAATTATGATTTTGAATAATATCCATTGCAACAAGTATAGATTAACTAG 900
Db 967 ATATTTTCCAATTATGATTTTGAATAATATCCATTGCAACAAGTATAGATTAACTAG 1026
Qy 901 GAAATTTATACAGATCCAGTGGGATTTTCAAGGGGAAATTTAGTGTGGCAACGTTTTTT 960
Db 1027 GAAATTTATACAGATCCAGTGGGATTTTCAAGGGGAAATTTAGTGTGGCAACGTTTTTT 1086
Qy 961 AGCTTAATTCGGTAGAGCAAAATGGAACAAGGGGACCTGGTTAGTTACTTGGCTTCAA 1020
Db 1087 AGCTTAATTCGGTAGAGCAAAATGGAACAAGGGGACCTGGTTAGTTACTTGGCTTCAA 1146
Qy 1021 GCTATAGATATATATATAGTCAATCTTATTAATCTTCACTTGGTTATCTTATGCTGGGG 1080
Db 1147 GCTATAGATATATATATAGTCAATCTTATTAATCTTCACTTGGTTATCTTATGCTGGGG 1206
Qy 1081 GGAACCTGTCATATATAGAACTTCAACAAAGGTTAAGGTCCTTTCAAGTATGCTCGA 1140
Db 1207 GGAACCTGTCATATATAGAACTTCAACAAAGGTTAAGGTCCTTTCAAGTATGCTCGA 1266
Qy 1141 ACTACAGATATATATATATATATATTTTGGCAATTCGATATATTTAAATTAAT 1200
Db 1267 ACTACAGATATATATATATATATATTTTGGCAATTCGATATATTTAAATTAAT 1326
Qy 1201 TCATTAAGTATATATATATATATATATTTTGGCAATTCGATATATTTAAATTAAT 1260
Db 1327 TCATTAAGTATATATATATATATATATTTTGGCAATTCGATATATTTAAATTAAT 1386
Qy 1261 TCACGGGCAAAATTTTTCGCAACAACATTAATCTTCTGATATAGGTTAAACGTTCT 1320
Db 1387 TCACGGGCAAAATTTTTCGCAACAACATTAATCTTCTGATATAGGTTAAACGTTCT 1446
Qy 1321 GGGTACTCAGACAAATTTGATCTGTGTACAGGATTAATTAAGGTTACACCACTAG 1380
Db 1447 GGGTACTCAGACAAATTTGATCTGTGTGTACAGGATTAATTAAGGTTACACCACTAG 1506
Qy 1381 CGTACAAATTTACTCTCATAGATTTATCAAAATGCGCATGTGTTCAAAATGAACCTCAGA 1440
Db 1507 CGTACAAATTTACTCTCATAGATTTATCAAAATGCGCATGTGTTCAAAATGAACCTCAGA 1566
Qy 1441 GTTAAAGTATTTGGTTGGACACATACAGATTAAGGTTAAATTTTCCAGAT 1500
Db 1567 GTTAAAGTATTTGGTTGGACACATACAGATTAAGGTTAAATTTTCCAGAT 1626
Qy 1501 AAAATTTACCAAAATTTCTGAGTAAGGTTTGGCCCTACACAGGTTACAGGATATGCA 1560
Db 1627 AAAATTTACCAAAATTTCTGAGTAAGGTTTGGCCCTACACAGGTTACAGGATATGCA 1686
Qy 1561 GGAAGTTACGTCACAGCTGGGCTGTGTTATACAGAGAGATAGTAAAGTTACCTTAT 1620
Db 1687 GGAAGTTACGTCACAGCTGGGCTGTGTTATACAGAGAGATAGTAAAGTTACCTTAT 1746
Qy 1621 CAAGCAAGTTTAAATTAAGTAACTTTGACACCAAGGATTAAGGTTACCTTAT 1680
Db 1747 CAAGCAAGTTTAAATTAAGTAACTTTGACACCAAGGATTAAGGTTACCTTAT 1806
Qy 1681 CTTCGCTACGCGAGTGAAGGACCTGGTCCGTTCCGATAGAAAGATGTTGCCAAGTTCT 1740
Db 1807 CTTCGCTACGCGAGTGAAGGACCTGGTCCGTTCCGATAGAAAGATGTTGCCAAGTTCT 1866
Qy 1741 GTTCAAAATGCTAATTTTCTGCTCAGCTACAGGTTAGTTCATTTGATTAATGTTG 1800

Db 1867 GTTCAAAATGCTAATTTTCTGCTCAGCTACAGGTTGCTATAGTTATGTTATGTC 1926
Qy 1801 GACACCTTAGTTACTATCATTTATATCAATCAGGTTGTAATAATTAATTAATCTATCT 1860
Db 1927 GACACCTTAGTTACTATCATTTATATCAATCAGGTTGTAATAATTAATTAATCTATCT 1986
Qy 1861 GGTATCCACCTTATGTTGACAAAGTGAATTTATCCCAATTTGACATCCAAATTTGAAAA 1920
Db 1987 GGTATCCACCTTATGTTGACAAAGTGAATTTATCCCAATTTGACATCCAAATTTGAAAA 2046
Qy 1921 TGTACGAATTTGCAATTTCCAGAGACATATGTAGATGTGAAGGATCAATCTTGGAA 1980
Db 2047 TGTACGAATTTGCAATTTCCAGAGACATATGTAGATGTGAAGGATCAATCTTGGAA 2106
Qy 1981 AAAAAAAAAAGATTGTAATATGTTATTTATCAATTA 2019
Db 2107 AAAAAAAAAAGATTGTAATATGTTATTTATCAATTA 2145

RESULT 3
ADR89416
ID ADR89416 standard; cDNA; 2010 BP.
XX
AC ADR89416;
XX
DT 18-NOV-2004 (first entry)
XX
DE AXMI-008 alternative start site coding sequence.
XX
XX ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
XX expression cassette; transformation; transgenic; plant; bacteria;
XX lepidoptera; coleoptera; pest; pesticide; resistance;
XX pesticidal activity.
XX OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT CDS 1..2010
FT /tag= a
FT /product= "Alternative AXMI-008"
XX
PN MO2004074462-A2.
XX
PD 02-SEP-2004.
XX
PE 20-FEB-2004; 2004MO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782147.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX
PA (ATHE-) ATHENIX CORP.
XX
PI Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;
XX
DR WPI; 2004-635574/61.
DR P-PSDB; ADR89417.
XX
PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
XX and polypeptides, useful for killing lepidopteran or coleopteran pests or
XX for producing organisms with pesticide resistance.
XX
PS Claim 1; SEQ ID NO 28; 178bp; English.
XX


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Cc      1861 CTTATTGTTGCAAGGCGAATTTATCCGATTGACATCCAAATTGAAAAATGTACGAAA 1920
Cc      1930 TGTCAATTCGAAGAGACATATGTAGTGTGAAGAGTACAAATCCTTGAAACAAAAAA 1989
Cc      1921 TGTCAATTCGAAGAGACATATGTAGTGTGAAGAGTACAAATCCTTGAAACAAAAAA 1980
Cc      1990 GAGATTGTAATAGTTATTTATTCATTA 2019
Cc      1981 GAGATTGTAATAGTTATTTATTCATTA 2010

RESULT 4
ID      ADR89401 standard; cDNA; 2082 BP.
XX      ADR89401;
XX      18-NOV-2004 (first entry)
XX      AXMI-008 coding sequence.
XX      se; gene: delta-endotoxin; delta-endotoxin associate polypeptide;
XX      expression cassette; transformation; transgenic; plant; bacteria;
XX      lepidoptera; coleoptera; pest; pesticide; resistance;
XX      pesticidal activity.
XX      OS      Bacillus thuringiensis.
XX      FH      Key      Location/Qualifiers
XX      FT      CDS      1..2082
XX      FT      /*tag= a
XX      FT      /product= "AXMI-008"
XX      FT      /transl_except= pos:1..3, aa:Met
XX      MO2004074462-A2.
XX      PD      02-SEP-2004.
XX      PF      20-FEB-2004; 2004MO-US005829.
XX      PR      20-FEB-2003; 2003US-0448632P.
XX      PR      20-FEB-2003; 2003US-0448633P.
XX      PR      20-FEB-2003; 2003US-0448797P.
XX      PR      20-FEB-2003; 2003US-0448806P.
XX      PR      20-FEB-2003; 2003US-0448810P.
XX      PR      20-FEB-2003; 2003US-0448812P.
XX      PR      19-FEB-2004; 2004US-00781979.
XX      PR      19-FEB-2004; 2004US-00782020.
XX      PR      19-FEB-2004; 2004US-00782096.
XX      PR      19-FEB-2004; 2004US-00782141.
XX      PR      19-FEB-2004; 2004US-00782570.
XX      PR      19-FEB-2004; 2004US-00783417.
XX      PA      (ATHE-) ATHENIX CORP.
XX      PI      Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B,
XX      DR      WPI; 2004-635574/61.
XX      DR      P-PSDB; ADR89402.
XX      PT      New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
XX      PT      and polypeptides, useful for killing lepidopteran or coleopteran pests or
XX      PT      for producing organisms with pesticide resistance.
XX      PS      Claim 1; SEQ ID NO 13; 178bp; English.
XX      CC      This sequence encodes an isolated delta-endotoxin. Some of the delta-
Cc      CC      endotoxin coding sequences of the invention have alternative start
Cc      CC      codons, producing more than one protein from a single open reading frame.
Cc      CC      The nucleic acid sequences of the invention are useful in DNA constructs
Cc      CC      or expression cassettes for transformation and expression in plants and
Cc      CC      bacteria. The nucleic acids and corresponding polypeptides are useful for
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Cc      Cc      killing lepidopteran or coleopteran pests. Compositions containing the
Cc      CC      delta-endotoxins of the invention, and methods for their production, are
Cc      CC      useful for the production of organisms with pesticide resistance,
Cc      CC      specifically bacteria and plants. These organisms are useful for
Cc      CC      generating altered or improved delta-endotoxin or delta-endotoxin-
Cc      CC      associated proteins that have pesticidal activity, or for detecting the
Cc      CC      presence of delta-endotoxin or delta-endotoxin-associated proteins or
Cc      CC      nucleic acids in products or organisms.
Cc      XX      Sequence 2082 BP; 699 A; 305 C; 434 G; 644 T; 0 U; 0 Other;
Cc      XX      Query Match      37.0%; Score 747.2; DB 13; Length 2082;
Cc      CC      Best Local Similarity 69.8%; Pred. No. 1.7e-179;
Cc      CC      Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7;

Cc      Cc      1 GTGAAAAATATGATTTCTTATCAAAATACAAATGAAATGAAATTCGTGATGTCCTCCG 60
Cc      CC      1 GTGAAAAATGATGATTCATATCAAAATGAAATGAAATGAAATTCGTGATGTCCTATCG 60
Cc      CC      61 AATTAACAATATGTCACAGATATCTTTTGCAGAGATCCAAATATATTTCTATT 120
Cc      CC      61 AATTAACAATATGTCACAGATATCTTTTGCAGAGATCCAAATATATTTCTATT 120
Cc      CC      121 AACCTGACGCTTGTCCAGGAAAGCCATGCAAGATACCTGCGAAATCAGTCTCGATATA 180
Cc      CC      121 TCTTGAATGATGTCAGGAAATCATGGAATGAAATTTGGGAATCAGTCGAAACGATA 180
Cc      CC      181 GTTACTATTTGGACATCTTATACAAATCTTGCTGTAACCCGCTATAGTGGAAATTCCT 240
Cc      CC      181 ACAAGTATGGAGATTAATCTTATAGATTTGATAGAACCTTAATTTGGGTGGAATTAAT 240
Cc      CC      241 GTTAATATTTCAATATATAAACAACCTATTCGCTCTGTCGTAATCTGTGGACAGACT 300
Cc      CC      241 ACACTTTATCAATATATAGAAAACTAATTCGACTAATGTCGTAACCTGTGACACTT 300
Cc      CC      301 TCTATATGATTTAGTATCTAATTCGTAAGAGTGAAGACAGACGCTGTAAAGTGAAC 360
Cc      CC      301 TCTATATGATTTATTTATCTAATTCGTAAGAGTGAAGACAGATGATTTTAAAGTGAAT 360
Cc      CC      361 GGGGTTGCAATTTTGAAGGCTGAATGATCTGCTTACAAATTTATTTCTTATCTT 420
Cc      CC      361 GCGATTGCAAGATTTTGAAGGCTGAATTTGAAATTTAAGAGATTAATCTTTCTTATCTT 420
Cc      CC      421 GAGGATTTGGCTTACG-----ATAATCAATCTTAAATCTTGTGAC 465
Cc      CC      421 GGGGCTTGGCTTAAAGACGTTAAACCACTTCAAAAGACAAATTAATCTGATATGACAA 480
Cc      CC      466 GTAGTTAAACAGTTCACAGCAGGAAAGAAATTTCACTAACTTTAGCAGGTCATTA 525
Cc      CC      481 TTAGTTATTTATTTTAACTTTCAAGAAAGATTTCAATGAATTTCTAGAGGGTCATTG 540
Cc      CC      526 TCAAGACAGAAAGCTGAATATTTATTTGCTAGTATGTCAGACTGCAATGTGCAT 585
Cc      CC      541 TCAAGAAACAAATGCTCAAGTATTTGTTATTTACCTTCTTGTGCAACAGCTCCAAATGTG 600
Cc      CC      586 TTATTACTATTAAGGAGCAGTTAATTAATAAAGAAATGGGGAATAGAGTGCACCG 645
Cc      CC      601 TTATTACTATTAAGGAGCAGTTAATTAATAAAGCAATATGTTCCATTTTGTAGTGCA 660
Cc      CC      646 TTGTATCCAGGCTCAGGAGAA-----CTGATGT 675
Cc      CC      661 GAGAAATGTAAGATCGAATTAATTAATCACTTAACAGTGTGATTTTACCGGTGATTC 720
Cc      CC      676 AACGACGGTGAAGCGAAATTAAGAGTATCTAATTTATTTGTAGGGTGTATTAAC 735
Cc      CC      721 TATGACCGATTAATAAGCAAAACGCGAGATATCCAAATATTTGTTATATTTATGAC 780
Cc      CC      736 AACGGTTTGAATAGTAAAGACAGCGGCTACAAAGTTCGAGTTTGTGCGAAATTAAT 795
Cc      CC      781 GTAGTTTAAATGATTAAGTAAACAGGGGGGACAGGGCTGACACTTGTGCGAAATTAAT 840
Cc      CC      796 AATTTCCGTAAGAAATGACGTTGGCGTATTTGATTAATTTGCTAATTTTCCAACTTAAT 855
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Db      841 AATTTGTAGAGAAATGACGTGGCGTATGTGATATATTCGCTATATTTCCAACTTAT 900
Qy      856 GATTTTGAAAAATATTCATTAGCAACAAGTGTAGATTAACTAGAGAAATTTATACAGAT 915
Db      901 GATTTTGAGAAATATTCATTAGCAACAAGTGTAGATTAACTAGAGAAATTTATACAGAT 960
Qy      916 CCAGTGGGATATTCAGGGGAAATTAATGTGGGAACGCTTT-----TTAGCTTTAAT 969
Db      961 GCAGTGGGATATTCAGGGGAAATTAATGTGGGAACGCTTTAAATTAATTAATTAAT 1020
Qy      970 TCGGTAGAGCAATAGGAAACAGCGGACCTGTTAGTACTTGGCTTCAAGTATATAGAT 1029
Db      1021 GGGTTAGAGGCTATATGAAACAGCGGACCTGTTAGTACTTGGCTTCAAGAAATATAGAT 1080
Qy      1030 ATATATATGCTATCTTATTAATCTTCAAGCTTGTATCTTACGTGGGGGGAACTCGT 1089
Db      1081 ATATATATATGAGTATGTT-----TCGAGATATTTTGGCGGCTGGGTAGGAACCTGT 1131
Qy      1090 CATTATGAAAGCTTCAAAAGGTTAAGGTCCTTTTCAACGTATGTCTGAACTACGAGAT 1149
Db      1132 CATTATGAAAGCTTCAAAAGGTTAAGGTCCTTTTCAACGTATGTCTGAACTACGAGAT 1191
Qy      1150 AATAATCCAGTAAATTAATTTATTTGGCAATACCGATATATTAATTAATTTATTTAGT 1209
Db      1192 AATGATCTAGCTATATTTGATTTTCAAGATCCGATGTATATTAATTAATTTACTTCAATAGCT 1251
Qy      1210 AGATATGCAATGCAACCGTTGTTGGTATTCATATCCACGCACTCTGTTTCACTGCA 1269
Db      1252 A---TCATGAAACCTAGTAGAGAGACACTACGCTAGACAGATATCGGTTTCAAAAGCA 1308
Qy      1270 GAATTTTTCGCAACAACCTAAATACCTTCTCTGATAGAGTAAACAGTTCTGGG---TAC 1326
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Qy      1327 TCACAGCAATGTAATCTGTGTTACCAAGTATTAAGATCTACCAACCTAGTCGTACA 1386
Db      1369 AGATGACAAATTAATTTAGCTTCCACTTGT-----ATTGCACTCTAAATGAGGTTAGA 1422
Qy      1387 AATTACTCTATAGATTATCAAAATGCGGATGTTGTTCAAAATGAAACCTCCAGAGTTAAC 1446
Db      1423 GGAACCTCTCATATATTAATTAATGCGGCAATGTTGTTATATGAAATCCAGAGTTAAC 1482
Qy      1447 GTATTTGGTGGACACATACAGTATGAAAAAGATTAATGCAATTTATCCAGATTAAT 1506
Db      1483 GTATATGTTGGACACATACAGTATTAACGTAATAATTAATTAAGCAATCAAT 1542
Qy      1507 ACGCAATTCCTGTCAGTAATAAGCTTTTGCCCTTACCAAGAGGTACAGATATGACGAGGT 1566
Db      1543 ACACAAATACCGGCGGTGAAGAGTTATTAATCTCAAAATTAATCTTGTAAATGCTATACC 1602
Qy      1567 TACGTCAACAGCTGGGCT 1584
Db      1603 TATGTATTAATAAGGCACT 1620

```

RESULT 5
 ADR89400 ID ADR89400 standard; cDNA; 5980 BP.

XX ADR89400;
 DT 18-NOV-2004 (first entry)
 XX AXMI-008 full length coding sequence.
 DE ss: gene: delta-endotoxin; delta-endotoxin associate polypeptide;
 XX expression cassette; transformation; transgenic; plant; bacteria;
 KM lepidoptera; coleoptera; pest; pesticide; resistance;
 XX pesticidal activity.
 OS *Bacillus thuringiensis*.
 XX Key Location/Qualifiers
 FH

```

FT      CDS      168..2249
FT      /*tag= a
FT      /product= "AXMI-008"
FT      /transl_except= pos:168..170, aa:Met
XX      W02004074462-A2.
PD      02-SEP-2004.
XX      20-FEB-2004; 2004MO-US005829.
PF      20-FEB-2003; 2003US-0448632P.
PR      20-FEB-2003; 2003US-0448633P.
PR      20-FEB-2003; 2003US-0448797P.
PR      20-FEB-2003; 2003US-0448806P.
PR      20-FEB-2003; 2003US-0448810P.
PR      20-FEB-2003; 2003US-0448812P.
PR      19-FEB-2004; 2004US-00781979.
PR      19-FEB-2004; 2004US-00782020.
PR      19-FEB-2004; 2004US-00782096.
PR      19-FEB-2004; 2004US-00782141.
PR      19-FEB-2004; 2004US-00782570.
PR      19-FEB-2004; 2004US-00783417.
XX      (ATHE-) ATHENIX CORP.
PA
XX      Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
PI      WPI; 2004-635574/61.
XX      P-PSDB; ADR89402.
DR
XX      New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT      and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT      for producing organisms with pesticide resistance.
XX      Claim 1; SEQ ID NO 12; 178bp; English.
PS
XX      This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC      endotoxin coding sequences of the invention have alternative start
CC      codons, producing more than one protein from a single open reading frame.
CC      The nucleic acid sequences of the invention are useful in DNA constructs
CC      or expression cassettes for transformation and expression in plants and
CC      bacteria. The nucleic acids and corresponding polypeptides are useful for
CC      killing lepidopteran or coleopteran pests. Compositions containing the
CC      delta-endotoxins of the invention, and methods for their production, are
CC      useful for the production of organisms with pesticide resistance.
CC      specifically bacteria and plants. These organisms are useful for
CC      generating altered or improved delta-endotoxin or delta-endotoxin-
CC      associated proteins that have pesticidal activity, or for detecting the
CC      presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC      nucleic acids in products or organisms.
XX      SQ      Sequence 5980 BP; 2018 A; 976 C; 1146 G; 1840 T; 0 U; 0 Other;

```

Query Match 37.0%; Score 747.2; DB 13; Length 5980;
 Best Local Similarity 69.8%; Pred. No. 2,4e-179;
 Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7;

```

Qy      1 GTGAAAAATATGAAATCTTATCAAAATGAAATGAAATTTCTGATGTTCCCG 60
Db      168 GTGAAAAAGATGATCATATCAAAATTAATAAGAAATATGAAATTTGGAATCCTCATCG 227
Qy      61 AATACACAAATATGTCAAACAGATATCTTTGCAAAAGATCAATATATTTCTATT 120
Db      228 AATACACAAATATGCGCAACAGATATCTTTGCAAAATATGGAATATGTTACTATAG 287
Qy      121 AACCTGACGCTTGTAGAGGAGCCATGCGCAAGATAGTGGGAATCACTGCGATATA 180
Db      288 TCTTGGAATGATGTCAGGGAATCTCATGGAATTTGGGAATCAGTCGAAAGATA 347
Qy      181 GTAAGTATGGGACATACCTTATACAAATCTTGTGAAACCGGTTAGGTGAATTCCT 240
Db      348 ACAAGTATGGGATTAATCTTATAGAGTTTGTATGAAACCTTATGTTGGTGAATTAAT 407

```


DT 04-JUL-2000 (first entry)
 XX Sequence encoding truncated Cry9Aa toxin.
 XX Cry9Aa; insecticide; transgenic plants; pest control; crop protection;
 XX ds.
 XX Synthetic.
 OS Bacillus thuringiensis; ssp. galleria.
 XX
 XX Key Location/Qualifiers
 FH CDS 17..1966
 FT /*tag= a
 FT /product= "Cry9Aa toxin N-terminal fragment"
 XX
 XX MO200011025-A1.
 XX
 XX 02-MAR-2000.
 XX
 XX 24-AUG-1999; 99MO-F1000698.
 XX
 XX 24-AUG-1998; 98FI-00001809.
 XX
 XX (UNIC-) UNICROP LTD.
 XX
 XX Kuvshinov V, Kanerova A, Koiyu K, Penu E;
 DR MPI: 2000-224660/19.
 DR P-PSDB; AA183039.
 XX
 XX Modified synthetic DNA sequences comprise modification of the truncated
 PT cry9Aa gene of Bacillus thuringiensis for improved insect control in
 PT plants.
 XX
 XX Claim 2, Page 55-57; 90pp; English.
 PS
 XX Synthetic DNA sequences derived from the sequence of the truncated cry9Aa
 CC gene of Bacillus thuringiensis ssp. galleria can be used for the
 CC production of a unique insecticidal protein having the same properties as
 CC the N-terminal domain of the insecticidal protein encoded by the native
 CC cry9Aa gene of Bacillus thuringiensis ssp. galleria. The insecticidal
 CC toxin works by binding to specific receptor molecules in the gut of
 CC insects with consequent formation of ion channels in the epithelium. This
 CC action leads to ion efflux and paralysis of the intestinal function. This
 CC which causes death of the insect. The synthetic DNA sequences exhibit
 CC enhanced expression through improved mRNA processing, stability, and/or
 CC translation providing improved tolerance against target insects. They can
 CC be used in the production of transgenic plants capable of expressing the
 CC N-terminal domain of the insecticidal protein encoded by the native
 CC cry9Aa gene. They therefore have a role in pest control and crop
 CC protection
 CC
 XX
 XX Sequence 1983 BP; 626 A; 340 C; 387 G; 630 T; 0 U; 0 Other;
 SQ
 Query Match 8.6%; Score 174; DB 3; Length 1983;
 Best Local Similarity 54.3%; Pred. No. 1,2e-33;
 Matches 441; Conservative 0; Mismatches 335; Indels 36; Gaps 3;

QY 395 ATCAAGATTATATCTTC-----ATTATCTTGAGAGATTGGCTTACAGATA 439
 DB 384 ACAGAACTATTATTAGAGCTCTGATAGCTGGAATAAGAACTCTATCTGCTTGC 443
 QY 440 AATCAAAATCCTAAAAAACCTTGCTGACGTATGATTAACAGTTCACAGACAGGAAGAAT 499
 DB 444 AAGAACTCCGTACTCGTTTAAATCCCGACTCAGAAATTGATAGAAATTTTAAACCCG 503
 QY 500 TCACTAACTTTTAAAGAGGTCATTATCAAGACAGAAAGCTGAAATTTATTATTGCTTA 559
 DB 504 GGTCTTTAAAGAAATGCTGCTGTTAGCTAGCAAAAATGCCAAATATTATTATTACCTT 563
 QY 560 CGTATCTGCAACCTGCAAAATGTCATTTATTTCTATTAAAGGACCCAGTTAAATATAAAA 619
 DB 564 CTTTTCGAGCGCTGATATTTCATTTATTACTTAAGGAGATCTACTAGATATGCA 623
 QY 620 AAGAAATGGGAACTAGTGTGTCACCGTTGTATCCAGGCTCAGGAGAACTGATTGTAAAG 679
 DB 624 CTAAATTTGGGGCTATATACAAATGCTACACCTTTATTA-----ATTATCAAT 668
 QY 680 AGCGGTTAAAGCGAAATATAAGATATCTAATTATTGTGTAGGGTATTAACAAG 739
 DB 669 CAAAACCTAGTAGCTTATTTGAACATATATAGATTAATTCGTAATGTAATTCGAG 728
 QY 740 GTTTAGATCAGATTAAGACAGCGGGTACAGAGCTGAAGTTGTGCAATTTAATTAAT 799
 DB 729 GTTTCACGAACTAAAGACAGAGGACATGATGCTACAGCTGTGTTAGAAATTCATAGAT 788
 QY 800 TTCTAGAGAAATGACGTTGGCGTATTTGATATTTATTTTCCAACTATGATTT 859
 DB 789 ATCTGATAGAGATGATGATTTGATATTTAGATATGATGATTTCAACTCTTGATA 848
 QY 860 TTGAAAATATTCATTTAGCAACAAGTATGATTAATTTAGGAAATTTATACAGATCCAG 919
 DB 849 TTACTAATTTACCAATAGAAACAGATTTTCACTGATGATGAGGCTCATTTATACAGATCCAA 908
 QY 920 TGGGATATTCAGGGGGAATTTATGTTGGGAA 951
 DB 909 TTGGTTTGTACATCGTAGTATGTTTAAAGGGA 940

RESULT 8
 AA293235
 ID AA293235 standard; DNA; 3837 BP.
 XX
 XX AA293235;
 AC
 XX
 XX 15-SEP-2003 (revised)
 DT 04-JUL-2000 (first entry)
 XX
 XX Sequence encoding native Cry9Aa toxin.
 XX
 XX Cry9Aa; insecticide; transgenic plants; pest control; crop protection;
 XX ds.
 XX Bacillus thuringiensis; ssp. galleria.
 OS
 XX Key Location/Qualifiers
 FH CDS 385..2364
 FT /*tag= a
 FT /product= "Cry9Aa toxin"
 XX
 XX MO200011025-A1.
 XX
 XX 02-MAR-2000.
 XX
 XX 24-AUG-1999; 99MO-F1000698.
 XX
 XX 24-AUG-1998; 98FI-00001809.
 XX
 XX (UNIC-) UNICROP LTD.
 XX

PI Kuvshinov V, Kanerva A, Koivu K, Pehu E;
 XX WPI, 2000-224660/19.
 DR P-PSDB; AAY82988.
 XX Modified synthetic DNA sequences comprise modification of the truncated
 PT cry9Aa gene of *Bacillus thuringiensis* for improved insect control in
 PT plants.
 XX Claim 10; Page 57-59; 90pp; English.
 XX
 XX Synthetic DNA sequences derived from the sequence of the truncated cry9Aa
 CC gene of *Bacillus thuringiensis* ssp. *galleria* can be used for the
 CC production of a unique insecticidal protein having the same properties as
 CC the N-terminal domain of the insecticidal protein encoded by the native
 CC cry9Aa gene of *Bacillus thuringiensis* ssp. *galleria*. The insecticidal
 CC toxin works by binding to specific receptor molecules in the gut of
 CC insects with consequent formation of ion channels in the epithelium. This
 CC action leads to ion efflux and paralysis of the intestinal function.
 CC which causes death of the insect. The synthetic DNA sequences exhibit
 CC enhanced expression through improved mRNA processing, stability, and/or
 CC translation providing improved tolerance against target insects. They can
 CC be used in the production of transgenic plants capable of expressing the
 CC N-terminal domain of the insecticidal protein encoded by the native
 CC cry9Aa gene. They therefore have a role in pest control and crop
 CC protection. (Updated on 15-SEP-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 3837 BP; 1279 A; 639 C; 791 G; 1128 T; 0 U; 0 Other;
 Query Match 8.6%; Score 174; DB 3; Length 3837;
 Best Local Similarity 54.3%; Pred. No. 1.6e-33;
 Matches 441; Conservative 0; Mismatches 335; Indels 36; Gaps 3;

QY 161 GGGATACGCTCCGATATAGTAACTATGAGCAATCTTATCAATCTTGTAGAAC 220
 DB 542 GCGATGACGAGAAAGAGCAATCTTATGAGCAACCAATGCTCTTATCAGAC 601
 QY 221 CCGGTATAGGTGAATCTCTGAATATTTT-----CAATATTAACAACATCTATTCGT 274
 DB 602 CTCTCTTACTGATTAATTAATTAATGATTAATGACCTTAATGTAAGTACTAGAGATA 661
 QY 275 CTTCGTGCAATCTGTGGAGCACTTCTATATGATTAATGATTAATGATTAATGATTAAG 334
 DB 662 GTAGTGAACATCAATCAATGATTTGCTATATGATTAATTAATTAATTAATTAATTAAT 721
 QY 335 AGGTAGACGAGAGCGTGAATGAGCGGGTTCAGATTTTGAAGGTGAATGACTCTT 394
 DB 722 GGGTAAGTCAGAGGTTTAAATGATGAGATTTTAAATGATTTTAAATGATTTTAAAT 781
 QY 395 ATCAAGATTATCTTC-----ATTATCTTGAGGATTTGCTTACAGATA 439
 DB 782 ACAGGAATCTATTAAGAGCTCTGATAGTGAATTAAGAAATCTTAATTTGCTTCTGCT 841
 QY 440 AATCAATTCCTAAAACTTGTGAGAGTGAATTAAGCGTTCCAGACCGGAGAGAT 499
 DB 842 AAGAACTCCGACTCGTTTGAATCCCGCACTCAGAAATTTGAAGATTTTAAACCGGAG 901
 QY 500 TCATTAACCTTTTACAGAGGCTATTAATCAAGACGAAGCTGAATTTATTTATTTGCTTA 559
 DB 902 GGTCTTTAAGGATTTGAGCTCGTTAGCTAGCAAAATGCCAAATTTATTTATTTACTT 961
 QY 560 CGTATGTGACAGCTGCAATGTGATTTATTAATTAAGGACGCGATTAATTAATTA 619
 DB 962 CTTTGTGAGCGCTGCAATTTTTCATTTATTAATTAAGGAGTGTACTAGATATGGA 1021
 QY 620 AAGAACTCCGACTCGTTTGAATCCCGCACTCAGAAATTTGAAGATTTTAAACCGGAG 679
 DB 1022 CTATTTGGGGGCTTAAATGCTTACACCTTTTATA-----ATTATTAAT 1066
 QY 680 AGCGTTTAAAGCGAAATTAAGAGTATTAATTTATTTGATGAGGTGATTAATTAAG 739
 DB 1067 CAATACTAGTAGAGCTTATTAATTAATTAATTTGATGAGGTGATTAATTAATTAAG 1126

QY 740 GTTATGATCAGATTAAGCAGCGCGGTACAAAGTCTGAAGTTGGTCGAATTAATTAAT 799
 DB 1127 GTTTCACGCACTTAAGCAAGAGGCACTGATGCTACAGCTTGTTGAATTTCAATGAT 1186
 QY 800 TTGATAGAAATGACGTTGGCGGTATTTGATATTTATTTGATTTTCAATTAATGAT 859
 DB 1187 ATGCTAGAGATGACATTTATGATTTATTAATTAATTAATTAATTAATTAATTAAT 1246
 QY 860 TTGAAAATATTCATTAAGCAACAGTGTAGAGTTAATTAAGGAAATTAATTAAGATCAG 919
 DB 1247 TTACTATTTACCAATTAAGAAACAGATTTTTCAGTTGATGATGATTTATTAATTAAT 1306
 QY 920 TGGGATTTTCAAGGCGGAAATTAATGTTGGGA 951
 DB 1307 TTGGTTTGTACATCGTAGTAGCTTTAGGGGA 1338

RESULT 9
 ID AAV16515 standard; DNA; 3471 BP.
 AC AAV16515;
 XX 11-JUN-1998 (first entry)
 DT
 XX DNA encoding a *Bacillus thuringiensis* toxin designated 86Bb1(a).
 DE
 XX Toxin; Lepidopteran pest; control; *Agrotis ipsilon*; black cutworm;
 KM *Heliothis virescens*; *Helicoverpa zea*; ss.
 KW
 XX *Bacillus thuringiensis*.
 FH Key Location/Qualifiers
 FT CDS 1..3471
 FT /tag= a
 XX
 PN W09800546-A2.
 XX
 PD 08-JAN-1998.
 PD
 XX
 PF 01-JUL-1997; 97MO-US011658.
 PR 01-JUL-1996; 96US-00674002.
 PA (MYCO) MYCOGEN CORP.
 PI
 XX
 PI Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
 XX
 DR WPI, 1998-086971/08.
 DR P-PSDB; AAW46856.
 XX
 PT New isolated *Bacillus thuringiensis* isolate(s) - used to obtain genes
 PT encoding toxins which are active against lepidopteran pests such as the
 PT Black cutworm.
 XX
 PS Example 5; Page 86-88; 183pp; English.
 PS
 XX
 CC The present sequence is isolated from a *Bacillus thuringiensis* isolate
 CC (PS6Bb1). It encodes a toxin designated 86Bb1(a) which is active against
 CC lepidopteran pests. The toxin isolates can be used for the control of
 CC lepidopteran pests such as *Agrotis ipsilon* (black cutworm), *Heliothis*
 CC *virescens* and *Helicoverpa zea*. PCR primers and probes can be derived from
 CC the polynucleotide encoding the toxin and used for the amplification and
 CC detection of other toxin-encoding sequences
 CC
 SQ Sequence 3471 BP; 1144 A; 591 C; 734 G; 1002 T; 0 U; 0 Other;
 Query Match 8.5%; Score 172.4; DB 2; Length 3471;
 Best Local Similarity 54.2%; Pred. No. 3.9e-33;
 Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 161 GGGATACGCTCCGATATAGTAACTATGAGCAATCTTATCAATCTTGTAGAAC 220

Db 158 GCGATGACGAAAGAGAGATATCTATTGGACAACATAGTCTCTTATCAGACAC 217
QY 221 CCGGATAGGTGGAATTCCTGTAATATTT-----CAATAATAACCAACTCATTCGGT 274
Db 218 CTTCTCTTACTGATTAATTTCAATAGATATAGACCTTAATAGGTAAGTACAGAGGTA 277
QY 275 CTTCTGATCATCTGGGACAGACTTCTATATGATTTAGATCATTAATTCGTAAG 334
Db 278 GTAGTGGACATCATATGAGATTTGTCTATATGATGACTTATATCTATTTATGATTTAC 337
QY 335 AGGTAGACGAGAGCGGTTAAGTACGCGGGTTCAGATTTTGAAGGTGAATGACTGCTT 394
Db 338 GGGTAGTACAGAGTGTTTAAATGATGAGGATGACAGTTTAAATGCTGACTCTTAT 397
QY 395 ATCAAGATTATATCTTC-----ATTATCTTGAGATGGCTTACAGATA 439
Db 398 ACAGGAATTAATTAAGGCTCTGGAATAGCTGGAATAGAAATCTTAATTCGCTTCGCTG 457
QY 440 AATCAAAATCTTAATAAACTTGACGTAAGTTAAACAGTCCAAAGCAGGGAAGAGATT 499
Db 458 AAGAACTCGGTACTCGTTTAAATGCGGACCTCAGAAATTTGATAGATTTTAAACCGAG 517
QY 500 TCACTAACTTTTACAGCGGTCTATATCAAGACAGAAAGCTGAATATTTATTTGCTTA 559
Db 518 GGTCTTTAAGCAATGGTGGCTCGTTAGCTAGACAAATGCCAAATATTAATTAATTA 577
QY 560 CGATGTGCAAGCTGCAAAATGTCATTTATTAATTAAGGAGCGAGTAAATATATAA 619
Db 578 CTTTTCGAGCGCTGCAATTTTCCATTTATTAATTAAGGATGCTACTAGATGATGGCA 637
QY 620 AAGAAATGGGACTAGTGTGTCCACCGTTATCCAGGGTTCAGGAGAACTGATTTGTAAG 679
Db 638 CTAAATTTGGGGGTATACAAATGCTAACACCTTTATAA-----ATTATCAAT 682
QY 680 AGCGGTTAAAGCGAAATTAAGAGATTAATTAATTTGTTGAGGTGTATTAACAAG 739
Db 683 CAAATCTAGTAGCTATATGAATATATCTATTAATTTGCTGTAATGATTAATCGAG 742
QY 740 GTTAGATCAGATTAAGACGCGGGGTACAGTCTGAAGTTTGCTGAATTTAATAAT 799
Db 743 GTTCAACGAACTTAAGCAACGAGGCTAGTGTCTCAGCTGTAGAAATTTCAATAGAT 802
QY 800 TTCTGAGAGAAATGAGCTGGCGGTATTTGATATTTATTTGCTATTTTCCAACTTATGATT 859
Db 803 ATCTGAGAGAGATGACATTTGATGATTAATAGATAGATCATTTTCAAGCTTGTATA 862
QY 860 TTGAAATATATCCATTAGCAACAAGTGTAGATTAACTAGGAAATTTATACAGATCCAG 919
Db 863 TTACTATATTACCAATTAAGAAACAGATTTTCAGTTGAGTAGGTCATTTATACAGATCAA 922
QY 920 TGGGATATTGAGGGGAAATTAATGTTGGGA 951
Db 923 TTGGTTTGTACATCGTAGTAGTCTTAAGGGA 954

RESULT 10
AAK83876
ID AAK83876 standard; DNA; 3471 BP.
XX
AC AAK83876;
XX
DT 09-SBP-1999 (first entry)
XX
DE Bacillus thuringiensis toxin 86Bb1(a) encoding DNA.
XX
KM Bacillus thuringiensis; toxin; Ostrinia nubilalis; lepidopteran;
XX European corn borer; black cutworm; ss.
OS Bacillus thuringiensis.
XX
PN WO933991-A2.
XX
PD 08-JUL-1999.

XX
PF 15-DEC-1998; 98WO-US026585.
XX
PR 31-DEC-1997; 97US-00002285.
XX
PA (MYCO) MYCOGEN CORP.
XX
PI Schepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
PI Muller-Cohn J;
DR WPI; 1999-40513/34.
DR P-PSDB; AAY24959.
XX
PT Method for control of European corn borer using Bacillus thuringiensis
toxins.
XX
PS Example 5; Page 90-92; 174pp; English.
XX
CC A method has been developed for the control of European corn borer
CC (Ostrinia nubilalis), comprising contacting the pest with a pesticidal
CC amount of a Bacillus thuringiensis toxin. The method is used for the
CC control of European corn borer (Ostrinia nubilalis). The method can also
CC be used for the control of other non-mammalian pests, particularly black
CC cutworm, and other lepidopteran pests. The present sequence encodes a
CC Bacillus thuringiensis toxin from the present invention
XX
SQ Sequence 3471 BP; 1144 A; 591 C; 734 G; 1002 T; 0 U; 0 Other;
Query Match 8.5%; Score 172.4; DB 2; Length 3471;
Best Local Similarity 54.2%; Pred. No. 3.9e-33;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;
QY 161 GGGATCACTCCGATATATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 220
Db 158 GCGATAGGTGGAATTCCTGTAATATTT-----CAATAATAACCAACTCATTCGGT 274
QY 221 CCGGATAGGTGGAATTCCTGTAATATTT-----CAATAATAACCAACTCATTCGGT 274
Db 218 CTTCTCTTACTGATTAATTTCAATAGATATAGACCTTATAGTAAAGTACAGAGGTA 277
QY 275 CTTCTGTCATCTGTGGACAGACTTCTATATGATTTAGATCTATTAATTTGTAAG 334
Db 278 GTAGTGGACAAATCCATATCAGATTTGTCTATATGACTTATTAATTAATTAATTA 337
QY 335 AGGTAGACGAGAGCGGTTAATGATGACGCGGTTCAGATTTTGAAGGTGAATGACTGCTT 394
Db 338 GGGTAGTACAGAGTGTTTAAATGATGAGGATTCAGATTTTAATGCTGTACTTAT 397
QY 395 ATCAAGATTATATCTTC-----ATTATCTTGAGATGGCTTACAGATA 439
Db 398 ACAGGAATTAATTAAGGCTCTGGAATAGCTGGAATAGAAATCTTAATTCGCTTCGCTG 457
QY 440 AATCAAAATCTTAATAAACTTGACGTAAGTTAAACAGTCCAAAGCAGGGAAGAGATT 499
Db 458 AAGAACTCGGTACTCGTTTAAATGCGGACCTCAGAAATTTGATAGAAATTTAAACCGAG 517
QY 500 TCACTAACTTTTACAGAGGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 559
Db 518 GGTCTTTAAGCAATGGTGGCTGTTAGCTAGCAAAATGCCAAATATTAATTAATTA 577
QY 560 CGATGTGCAAGCTGCAAAATGTCATTTATTAATTAATTAATTAATTAATTAATTAATTA 619
Db 578 CTTTTCGAGCGCTGATTTTCCATTTATTAATTAATTAATTAATTAATTAATTAATTA 637
QY 620 AAGAAATGGGACTAGTGTGTCCACCGTTGATCCAGGCTCAGGAGAACTGATTTGTAAG 679
Db 638 CTAAATTTGGGGCTAATCAATGCTAACCTTTATAA-----ATTATCAAT 682
QY 680 AGCGGTTAAAGCGAAATTAAGAGATTAATTAATTTGTTGAGGTGTATTAACAAG 739
Db 683 CAAATCTAGTAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 742
QY 740 GTTAGATCAGATTAAGACAGCGGGGTACAAAGTGTGAAGTTTGTGCAATTTAATAAT 799

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Db 743 GTTTCACGAACTTAAGACAGAGCCATTGCTACAGCTTGGTAGAATTTCAATGAT 802
Qy 800 TTCTAGAGAAATGACGTTGGCGGATTTGATATTTATTTCCATTATGAT 859
Db 803 ATCGTAGAGAGATGACATTTGATATTTAGATATTTAGATATTTTCAAGTCTGATA 862
Qy 860 TTGAAAAATATCCATTAGCAACAAAGTGAAGTTACTAGGAAATTTATACAGATCCAG 919
Db 863 TTACTAATTTACCCATATGAAACAGATTTTCAGTTGAGAGGATCATTTATACAGATCCAA 922
Qy 920 TGGATATTTGAGGGGAAATATGTTGGGAA 951
Db 923 TTGGTTTGTATCATCGTAGTAGTCTTAGGGGA 954

RESULT 11
AAS02478
ID AAS02478 standard; DNA; 2407 BP.
AC AAS02478;
AT 29-AUG-2001 (first entry)
DE B. thuringiensis DNA encoding a toxic crystal protein, CryET60.
XX
XX Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
XX transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum;
XX sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
XX pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
XX cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
XX cotton leaf perforator; CryET60; ds.
XX
XX Bacillus thuringiensis.
XX
XX Key Location/Qualifiers
XX CDS 1..2406
XX FT /*tag= a
XX FT /product= "CryET60"
XX FT /partial
XX FT /note= "No stop codon"
XX
XX MO200119859-A2.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000WO-US025361.
XX
XX 15-SEP-1999; 99US-0153995P.
XX
XX (MONS ) MONSANTO CO.
XX
XX PA
XX PI Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;
XX XX WPI; 2001-281518/29.
XX DR P-PSDB; AAU02035.
XX
XX Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
XX PT and the polynucleotides that encode them, useful for increasing the
XX insect resistance of plant.
XX
XX Claim 17; Page 127-128; 173pp; English.
XX
XX The sequence encodes a B. thuringiensis lepidopteran-active delta-
XX endotoxin, crystal protein CryET60. The lepidopteran-active B.
XX thuringiensis delta-endotoxin polypeptides may be used as compositions
XX CC that are applied to plant crops to protect them from insect damage. The
XX CC polynucleotides may be used in the production of transgenic plants that
XX CC express the insecticidal polypeptides and consequently have improved
XX CC insect resistance compared to non-transformed plants. Monocotyledonous or
XX CC dicotyledonous plants may be protected in this way, for example corn,
XX CC wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
XX CC tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,

```

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CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
CC cotton leaf perforator and spruce budworm) may be affected by application
CC of the insecticidal polypeptides (full details given in specification)
XX
XX Sequence 2407 BP; 785 A; 409 C; 495 G; 718 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 162.8; DB 4; Length 2407;
XX Best Local Similarity 53.4%; Pred. No. 9.4e-31;
XX Matches 434; Conservative 0; Mismatches 342; Indels 36; Gaps 3;
XX
Qy 161 GGGATATGCTCGATATAGTACTATTTGGAGATACCTTATACATTTCTGTAGAAC 220
Db 158 GCGATGAGCAAAAAGAGCATATCTATTTGGACAAACATAGTCTCTTATACAGAAC 217
Qy 221 CCGGTATAGGTGGAATTCCTGTATATTTT-----CAATATTAACAACTACATTCGCT 274
Db 218 CTTCTCTTACTGAGATTTAATTTCAATAGTATATGACCTTATAGGTAAGTACTAGAGGTA 277
Qy 275 CTTCTGTCATATCTGTGGACAGCACTTCTATATGTATATAGTATCTATATTTGTAAG 334
Db 278 GTAGTGAACAATCCATATCAGATTTGTCTATATGTGACTTATATTTATTTGATTTAC 337
Qy 335 AGTAGACAGAGCGGTATATAGTACGGGGTTGCAATTTTGAGCGGTAATGACTGCTT 394
Db 338 GGGTATCTCAGAGAGTTTAAATATGATGAGATTTGACAGATTTTAAATGTTCTGTACTTAT 397
Qy 395 ATCAAGATTTATATCTTC-----ATTATCTGAGATTTGGCTTACAGATA 439
Db 398 ACAGAACTTTTATAGAGCTCTGTATAGCTGGAATTAAGATCTTAATTTCTGCTGTG 457
Qy 440 AATCAAACTCTTAAAAAACTTGCTGACCGTAGTTAAACAGTTCCAAACAGGAGAAAGATT 499
Db 458 AAGAACTCCGTAACCTGTTTAAATGATGCCGACCTAGAAATTTAGATATTTTAACCGAG 517
Qy 500 TCACTAACTTTTATAGAGGCTCATTTCAAGACAAAGCTGAATATTTATTTGCTTA 559
Db 518 GGTCTTTTAAAGAAATGAGTGGCTCGTTAGCTAGACAAATATGCCAAATTTATTTACTCTT 577
Qy 560 CGTATGTGCAAGCTGCAAAATGTGCTATTTATTAAGGAGCGAGTTAAATATATAA 619
Db 578 CTTTGGAGCGCTGCAATTTTCCATTTATTTACTTAAAGGATGCTACTAGATATAGCA 637
Qy 620 AAGATGGGAGCTAGTGTGTCCACCGTTGTATCCAGGGCTCAGGAGAACTGATTTGTAAG 679
Db 638 CTAATTTGGGGCTATACAAATGTACACCTTTTATA-----ATTATCAAT 682
Qy 680 AGCGTTTAAAGCAAAATTAAGATATCTAATTTTGTGTAGGGTGTATTAACAAG 739
Db 683 CAAAACCTAGTAGAGCTTATTTGAATCTATATCTGATTTATTCGTACATTTGGGATTAATCGAG 742
Qy 740 GTTTAGATCAGATTAAGACAGGCGGGTACAGTGTCAAGTTTGGTGCAGAAATTTAATAAT 799
Db 743 GTTCAACCGAATTAAGACAGAGGCGCTTAGTGTCTACAGCTTGTTGAATTTATATGAT 802
Qy 800 TTCTAGAGAAATGACGTTGGCGGATTTGATATTTATTTTCCATTATGAT 859
Db 803 ATCGTAGAGAGATGACATTTGATATTTAGATATTTAGATATTTTCAAGTCTGATA 862
Qy 860 TTGAAAAATATCCATTAGCAACAAAGTGAAGTTACTAGGAAATTTATACAGATCCAG 919
Db 863 TTACTAATTTACCCATATGAAACAGATTTTCAGTTGAGAGGATCATTTATACAGATCCAA 922
Qy 920 TGGATATTTGAGGGGAAATATGTTGGGAA 951
Db 923 TTGGTTTGTATCATCGTAGTAGTCTTAGGGGA 954

RESULT 12
AEA61394
ID AEA61394 standard; DNA; 4391 BP.
AC AEA61394;

```

```
XX 11-AUG-2005 (first entry)
DT
XX Bacillus thuringiensis Cry19a coding sequence, SEQ ID 4.
DE
XX Insecticide; crystal protein; Cry19a; gene; ds.
XX
XX Bacillus thuringiensis.
OS
XX
XX Key Location/Qualifiers
FT CDS 719..2665
FT /tag= a
FT /product= "Cry19a"
XX
XX US2005124803-A1.
XX
XX 09-JUN-2005.
XX
XX 30-AUG-2004; 2004US-00929754.
XX
XX 29-AUG-2003; 2003US-0498826P.
XX
XX (OHIS ) UNIV OHIO STATE RES FOUND.
XX
XX Dean DH, Abdullah MA;
XX
XX WPI; 2005-417057/42.
XX
XX P-SDB; AEA61393.
XX
XX EMBL; Y07603.
XX
XX
XX New modified Bacillus thuringiensis insecticidal crystal proteins (i.e.
XX PT Cry4a and Cry19a) with enhanced toxicity, useful for reducing or
XX PT eliminating populations of target insects (i.e. mosquitoes) that are
XX PT vectors of disease.
XX
XX Disclosure; SEQ ID NO 4; 63bp; English.
XX
XX PS
XX
XX The present invention relates to modified insecticidal Bacillus
XX CC thuringiensis crystal proteins Cry4a and Cry19a which have enhanced
XX CC toxicity against a variety of insects, e.g. mosquitoes and lepidoptera.
XX CC The modified proteins are useful for reducing or eliminating populations
XX CC of target insects that are vectors of disease, particularly mosquitoes.
XX CC The present sequence is the coding sequence of the wild-type Cry19a
XX CC protein, which can be modified with: a substitution of amino acids at
XX CC positions 355 through 358 with amino acids tyrosine, glutamine, aspartic
XX CC acid, and leucine; an insertion of at least one amino acid (e.g.
XX CC arginine) after position 358 and a deletion of the amino acids at
XX CC positions 414 through 418.
XX
XX SQ Sequence 4391 BP; 1557 A; 630 C; 914 G; 1290 T; 0 U; 0 Other;
XX
XX Query Match 6.6%; Score 133.6; DB 14; Length 4391;
XX Best Local Similarity 48.1%; Pred. No. 3.2e-23;
XX Matches 720; Conservative 0; Mismatches 704; Indels 74; Gaps 9;
XX
XX 540 TGAATATATATATGCTACGTATGCAAGCTGCAAAATGTCATTATTAATTAG 599
XX 1303 TGAATATATATATGCTACGTATGCAAGCTGCAAAATGTCATTATTAATTAG 1362
XX
XX 600 GAGACGAGTTAAATATATATATATATATATATATATATATATATATATAT 659
XX 1363 GAGACGAGTTAAATATATATATATATATATATATATATATATATATATAT 1407
XX
XX 660 AGGAGACGAGTTATATATATATATATATATATATATATATATATATATAT 719
XX 1408 TGCTCGATATATATATATATATATATATATATATATATATATATATATAT 1467
XX
XX 720 TGTAGAGTGTATATATATATATATATATATATATATATATATATATATATAT 779
XX 1468 TATATATATATATATATATATATATATATATATATATATATATATATATAT 1516
XX
XX 780 TTGTCGAAATATATATATATATATATATATATATATATATATATATATAT 839
XX 1517 TGGTAAACCTTAATCGTTATCGTAGAGAAATGACTCTTACTGATTATATATAT 1575
XX 840 TATATTTCAACTTATATATATATATATATATATATATATATATATATATAT 899
XX 1576 AATGTTCCCTATATATATATATATATATATATATATATATATATATATAT 1635
XX
XX 900 GGAATATATATATATATATATATATATATATATATATATATATATATATAT 959
XX 1636 GGAATATATATATATATATATATATATATATATATATATATATATATAT 1692
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XX 960 TACCTTAAATTCGTATATATATATATATATATATATATATATATATATAT 1019
XX 1693 TCTCTTGAAGAAAGCGAATCACTTATATATATATATATATATATATATAT 1752
XX
XX 1020 AGCTATATATATATATATATATATATATATATATATATATATATATATAT 1079
XX 1753 AGAATTTGATTTGTAACCAATTTATATATATATATATATATATATATATAT 1812
XX
XX 1080 GGAACCTCGTCAATATATATATATATATATATATATATATATATATATAT 1139
XX 1813 TAAATATTTCTTATATATATATATATATATATATATATATATATATATAT 1872
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XX 1140 AACTACGATATATATATATATATATATATATATATATATATATATATAT 1196
XX 1873 AGATATATGTTGGAAGCTTCTTACCAATATATATATATATATATATATATAT 1932
XX
XX 1197 TATTTCAATAGCTATATATATATATATATATATATATATATATATATAT 1253
XX 1933 ATGACGGAATATATATATATATATATATATATATATATATATATATATAT 1992
XX
XX 1254 TCTTTGTCACGTGCAATATATATATATATATATATATATATATATATATAT 1313
XX 1993 GAATTTTCTGTAACGATATATATATATATATATATATATATATATATATAT 2052
XX
XX 1314 CAGTTCTGATCTACACAGCAATATATATATATATATATATATATATATAT 1373
XX 2053 GAATTAACCTGTTGTCGACAGATATATATATATATATATATATATATATAT 2112
XX
XX 1374 AACTATCGTACAAATATATATATATATATATATATATATATATATATATAT 1427
XX 2113 AGCAAAATATATATATATATATATATATATATATATATATATATATATAT 2172
XX
XX 1428 ---TGAACCTCGAGATTAAGTATATATATATATATATATATATATATAT 1484
XX 2173 TGGTCAAGAACGATATATATATATATATATATATATATATATATATATAT 2232
XX
XX 1485 TCGAATTTATCGAATATATATATATATATATATATATATATATATATAT 1544
XX 2233 TACCATTTGACGGAATATATATATATATATATATATATATATATATATAT 2292
XX
XX 1545 AGTACAGATATATATATATATATATATATATATATATATATATATATAT 1604
XX 2293 ATCGATTTCAATGAAAAGT-----CCCGAATTTACGGAGAGAAATTT 2337
XX
XX 1605 AGTACGTTACCTTATCAAGCAAGTTTAAATATATATATATATATATATAT 1664
XX 2338 GGTAAAGATGAGACGATATATATATATATATATATATATATATATATATAT 2397
XX
XX 1665 AATTTACGTTTGAATCTTCTGCTACGCGAGTGAAGACCTGTCCGTTCCGAGTAAAG 1724
XX 2398 AATATATCGTTTGAATCGTTATATATATATATATATATATATATATATAT 2457
XX
XX 1725 ATGG---TGGCAAGTTCTGTTTCAATATATATATATATATATATATATAT 1781
XX 2458 ATGAAAGGGGAGGTTATATATATATATATATATATATATATATATATATAT 2517
XX
XX 1782 TAGTCATTTGATTTATGAGACCTTATATATATATATATATATATATATAT 1841
XX 2518 CTTTCTTATTTAGAGCTTTTATATATATATATATATATATATATATATAT 2577
XX
XX 1842 AATTTATCAAAATCTATCTGTTTACACCTTATATATATATATATATATAT 1901
XX 2578 GAGAGTAAATATCTGATGATGACAGTTTGTGAAGATATATATATATATAT 2637
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QY 1902 TGACATCCAAATGTAAGAAATGTCATTCAGAGACATATGTAGATGCA 1961
 DB 2638 TAAATAGAAATTCCTCCCACTAGTACCATTCACA-----GGAAATATGCA 2686
 QY 1962 AGAGATCAATCTCTGGAAACAAAAGAGATTGTAATGTTATTTATCAATTAA 2019
 DB 2687 GGAATAATATGAAATTAGAAAGATCAGAGAAACATTATATATTTGTTATTA 2744

RESULT 13
 AAS02466
 ID AAS02466 standard; DNA; 1959 BP.
 XX AAS02466;
 AC AAS02466;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE B. thuringiensis DNA encoding a toxic crystal protein, CryET43.
 XX
 KM Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
 KM transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum;
 KM sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
 KM pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
 KM cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
 KM cotton leaf perforator; CryET43; ds.
 XX
 OS Bacillus thuringiensis.
 XX
 FH Key Location/Qualifiers
 FT 1..1959
 FT /*tag= a
 FT /product= "CryET43"
 FT /partial
 FT /note= "No stop or start codon"
 XX
 PN MO200119859-A2.
 XX
 PD 22-MAR-2001.
 XX
 PF 13-SEP-2000; 2000WO-US025361.
 XX
 PR 15-SEP-1999; 99US-0153995P.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;
 XX
 DR WPI: 2001-281518/29.
 DR P-PSDB; AAU02023.
 XX
 PT Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
 PT and the polynucleotides that encode them, useful for increasing the
 PT insect resistance of plant.
 XX
 PS Claim 17; Page 105; 173pp; English.
 XX
 CC The sequence encodes a B. thuringiensis Lepidopteran-active delta-
 CC endotoxin, crystal protein CryET43. The Lepidopteran-active B.
 CC thuringiensis delta-endotoxin polypeptides may be used as compositions
 CC that are applied to plant crops to protect them from insect damage. The
 CC polynucleotides may be used in the production of transgenic plants that
 CC express the insecticidal polypeptides and consequently have improved
 CC insect resistance compared to non-transformed plants. Monocotyledonous or
 CC dicotyledonous plants may be protected in this way, for example corn,
 CC wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
 CC tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
 CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
 CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
 CC cotton leaf perforator and spruce budworm) may be affected by application
 CC of the insecticidal polypeptides (full details given in specification)
 CC
 XX Sequence 1959 BP; 646 A; 348 C; 393 G; 572 T; 0 U; 0 Other;

Query Match 5.9%; Score 119.8; DB 4; Length 1959;
 Best Local Similarity 55.0%; Pred. No. 7.6e-20;
 Matches 294; Conservative 0; Mismatches 217; Indels 24; Gaps 2;

QY 435 AGATTAATCAATCTCTGAAACAACTGTCAGCGTGTAAACAGTTCCAGACGGGANA 494
 DB 411 AGATTAACCGAAGATCAAGATCAAGACATATTTCTGAGCGCTATGTGCTTTAGA 470
 QY 495 AGATTTCACTAACTTTTACAGGGGTCATTATCAAGACAGAAAGCTGAAATATTTATT 554
 DB 471 ACTTGACATTAACACTCTATACCGCTTTTCAGAAATCGAAATAGAAAGCTCATTTAT 530
 QY 555 GCTTACGTATGTGCAAGCTGCAAAATGTCATTTATTAATAAGGAGCGCATTTAATA 614
 DB 531 AATGTATATGCTCAAGCTGCAAAATTTACACCTATTTATTTAGAGACCATCCCTTT 590
 QY 615 TAAAAAAGATGGGGACTAGTGTCTCCACCGTGTATCCAGGGTCAGGAGAACTGATTG 674
 DB 591 TGGTAGTAATGGGGATGGCATCTTCGATGTTAACCA-----TA 632
 QY 675 TAAAGAGCGGTTAAAGCGAAATTAAGAGTACTAATTTATTTGTAGGGTGTATTA 734
 DB 633 TTACAGGAACAAATCGATATACAGAGAAATTTCTAACCATTTGCTCAATGTATTA 692
 QY 735 CAAGGTTTATGATCAGATTAAGACAGCGGGTACAGTGTGAAGTTGTGCAAAATTTAA 794
 DB 693 TACAGGGCTAAATVAACTTAAGA-----GGACAAATGTCTGAAGTTGGTGGCGTATTA 746
 QY 795 TAAATTTCTAGAGAAATGACGTTGGGGTATTTGATATTTATTTGCTATATTTCCACTTA 854
 DB 747 TCAATTCCTGAGAGACCTTAACGTTAGGGGTATTAAGTTGTGTCCTATTTCCACACTA 806
 QY 855 TGAATTTGAAATATTCATTTAGCAACAAGTGTAGATTAAGTAAAGGAAATTTTACAGA 914
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 QY 915 TCCAGTGGATATTCAGGGGAAATTAATGTTGGGAACGGTTTATTTAGCTTTAAT 969
 DB 867 TCCAAATGGAGAAACAAATGCACCTTCAGATTTTGAAGTACGAATGTTTAAAT 921

RESULT 14
 ADR89411
 ID ADR89411 standard; cDNA; 1986 BP.
 XX
 AC ADR89411;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE AXMI-009 alternative start site coding sequence #2.
 XX
 KM seq. gene; delta-endotoxin; delta-endotoxin associate polypeptide;
 KM expression cassette; transformation; transgenic plant; bacteria;
 KM lepidoptera; coleoptera; pest; pesticide; resistance;
 KM pesticidal activity.
 XX
 OS Bacillus thuringiensis.
 XX
 FH Key Location/Qualifiers
 FT 1..1986
 FT /*tag= a
 FT /product= "Alternative AXMI-009 #2"
 XX
 PN WO2004074462-A2.
 XX
 PD 02-SEP-2004.
 XX
 PF 20-FEB-2004; 2004WO-US005829.
 XX
 PR 20-FEB-2003; 2003US-0448632P.
 PR 20-FEB-2003; 2003US-0448633P.
 PR 20-FEB-2003; 2003US-0448797P.

PR 20-FEB-2003; 2003US-0448806P.
 PR 20-FEB-2003; 2003US-0448810P.
 PR 20-FEB-2003; 2003US-0448812P.
 PR 19-FEB-2004; 2004US-00781979.
 PR 19-FEB-2004; 2004US-00782020.
 PR 19-FEB-2004; 2004US-00782096.
 PR 19-FEB-2004; 2004US-00782141.
 PR 19-FEB-2004; 2004US-00782570.
 PR 19-FEB-2004; 2004US-00783417.
 (ATHE-) ATHENIX CORP.
 PI Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;
 XX MPI: 2004-635574/61.
 DR P-PSDB; ADR89412.
 XX
 PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 PT for producing organisms with pesticide resistance.
 XX
 PS Claim 1; SEQ ID NO 23; 178bp; English.
 XX
 CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
 CC endotoxin coding sequences of the invention have alternative start
 CC codons, producing more than one protein from a single open reading frame.
 CC The nucleic acid sequences of the invention are useful in DNA constructs
 CC or expression cassettes for transformation and expression in plants and
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for
 CC killing lepidopteran or coleopteran pests. Compositions containing the
 CC delta-endotoxins of the invention, and methods for their production, are
 CC useful for the production of organisms with pesticide resistance,
 CC specifically bacteria and plants. These organisms are useful for
 CC generating altered or improved delta-endotoxin or delta-endotoxin-
 CC associated proteins that have pesticidal activity, or for detecting the
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
 CC nucleic acids in products or organisms.
 XX
 XX Sequence 1986 BP; 659 A; 310 C; 395 G; 622 T; 0 U; 0 Other;
 Query Match 5.9%; Score 118.4; DB 13; Length 1986;
 Best Local Similarity 51.3%; Pred. No. 1,7e-19;
 Matches 544; Conservative 0; Mismatches 426; Indels 90; Gaps 8;

Db 916 ACTTACCCTTGATATATCTATATAACACCTTACGCTATGGAATAACGGAACA 975
 Qy 991 CGGGACCTGGTTTGGTTAGTTACCTGGCTCAAGCTATAGATATATATGTCATTCTATTAAT 1050
 Db 976 CGACGCTCTTCTTATACCACTTGGCTTATCTATTTTGTATATACAGACCTAGGCT 1035
 Qy 1051 CTTCAGCTGGTTATCTTATGAGGCTGGGGGGAACCGTCATTTATGAAGACTTCCAAAG 1110
 Db 1036 AATATGCTGATGTGGAATAATTTTGGGAGGCACTACATTAGTTGAATAAGAAATGAT 1095
 Qy 1111 GGTAACGCTGCTTTTCAACGTATGTCGAACTACAGATATATATCCAGT---AATAT 1167
 Db 1096 GGTTCTGAATATACCACTATACCTTGGTAAACTGATTCATTACTCTATTCATATTTT 1155
 Qy 1168 ATTTTGGCAATACCGATATATTTAAATTATTTCTATTAGCTAG-----ATATGCATG 1221
 Db 1156 AATTTGCGAACCCTTCTGTTTTCAGTATGTAGTCACTTCTGTATATATTTAGAGAGA 1215
 Qy 1222 CAACGTTTGGTGGATTCATATCCACAGGCATCTTGTTCACGTGCAAGATTTTTCGG 1281
 Db 1216 ACHAGAGCTAATATATATTTACTAGTCAGTATGAGTCTCGAGATTATTTTATACA 1275
 Qy 1282 ACAACACTAATA-----CTTTCGTATGAGTAAACAGTTCGGTACTCA 1329
 Db 1276 TCAATATATATATATATGATACCTGATCTTAAAGATGGAAGTGCCTGCTAATCTTCATCC 1335
 Qy 1330 CAGACATTAATCTGTGTATACAGATATATTAAGATCTACACTTATGCTGTACAAT 1389
 Db 1336 CAACCTATATTTTTCGAATTTACAGAAAGGATAG---CAAGACCAAAACGAGAGAT 1392
 Qy 1390 TACTCTCATAGATTTTCAATGCGGATGTGTCA-----AAATGAA 1431
 Db 1393 TTACGCAATAGATTTATCTTATATCAATTTTATGACAGCGGAAGTATCTCAGCGGT 1452
 Qy 1432 ACCTCAGAGTTAAAGTATTTGGTTGGACACATACAAAGTATGAAAAAGATATCAAT 1491
 Db 1453 ATTGTTAGCTTTTAAAGTGTGGTGGGCACTACAGATATGATGCTATATATGCTCT 1512
 Qy 1492 TATCCAGATTAATTAAGCAAAATTCCTGCACTAAAGCTT 1531
 Db 1513 GAACCAATTAATTAATCTCAAAATGATGACGTTAAAGGTT 1552
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 ID ADR89409 standard; cDNA; 2016 BP.
 AC
 AC ADR89409;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE AXMI-009 alternative start site coding sequence.
 DE
 KW sb; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
 KW expression cassette; transformation; transgenic; plant; bacteria;
 KW lepidoptera; coleoptera; pest; pesticide; resistance;
 KW pesticidal activity.
 XX
 OS Bacillus thuringiensis.
 XX
 FH Key Location/Qualifiers
 FT 1..2016
 FT CDS /tag= a
 FT /product= "Alternative AXMI-009"
 PN
 PD MO2004074462-A2.
 XX
 PD 02-SEP-2004.
 XX
 XX 20-FEB-2004; 2004WO-US005829.
 PF
 XX 20-FEB-2003; 2003US-0448632P.
 XX

Page 10 (10/10)

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OM nucleic - nucleic search, using sw model

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Maximum DB seq length: 2000000000

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	747.2	37.0	2082	8	US-10-781-979-2
5	747.2	37.0	5980	8	US-10-781-979-1
6	739.8	36.6	2073	8	US-10-781-979-4
7	172.4	8.1	3471	5	US-10-099-285-71
8	162.8	8.1	2407	6	US-10-428-961-29
9	133.6	6.6	4391	9	US-10-929-754-4
10	119.8	5.9	1959	6	US-10-428-961-5
11	117.6	5.8	1806	8	US-10-782-020-4
12	117.6	5.8	1890	8	US-10-782-020-2
13	116.8	5.8	2190	8	US-10-782-020-1
14	116.8	5.8	3684	6	US-10-428-961-62
15	113.4	5.6	2019	7	US-10-665-460A-7
16	112.4	5.6	3687	7	US-10-665-460A-7
17	112.4	5.6	4173	6	US-10-428-961-37
18	111.8	5.5	2019	7	US-10-665-460A-1
19	111.8	5.5	2019	7	US-10-665-460A-3
20	111.8	5.5	3471	5	US-10-099-285-73
21	111.8	5.5	3471	5	US-10-428-961-27
22	111.8	5.5	4344	9	US-10-687-879A-4
23	110.8	5.5	1561	9	US-10-687-879A-2

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25	105.4	5.2	2019	7	US-10-665-460A-11	Sequence 11, Appl
26	105	5.2	1860	5	US-10-032-717-19	Sequence 19, Appl
27	105	5.2	1860	6	US-10-414-637-19	Sequence 19, Appl
28	105	5.2	1860	7	US-10-606-320-15	Sequence 15, Appl
29	105	5.2	1860	8	US-10-746-914-15	Sequence 15, Appl
30	105	5.2	2003	5	US-10-032-717-5	Sequence 5, Appli
31	105	5.2	2003	6	US-10-414-637-5	Sequence 5, Appli
32	105	5.2	2010	5	US-10-032-717-15	Sequence 15, Appl
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36	105	5.2	3621	5	US-10-032-717-1	Sequence 1, Appli
37	105	5.2	3621	6	US-10-414-637-1	Sequence 1, Appli
38	105	5.2	3621	7	US-10-606-320-1	Sequence 1, Appli
39	105	5.2	3621	8	US-10-746-914-1	Sequence 1, Appli
40	105	5.2	3621	10	US-11-021-115-5	Sequence 5, Appli
41	105	5.2	4874	5	US-10-032-717-27	Sequence 27, Appl
42	105	5.2	4874	6	US-10-414-637-27	Sequence 27, Appl
43	105	5.2	4874	7	US-10-606-320-17	Sequence 17, Appl
44	105	5.2	4874	8	US-10-746-914-17	Sequence 17, Appl
45	104.4	5.2	3687	8	US-10-809-953-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-10-782-141-2
Sequence 2, Application US/10782141
Publication No. US20040197917A1
GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine
APPLICANT: Hargis, Tracy
APPLICANT: Koziel, Michael G.
APPLICANT: Duck, Nicholas B.
APPLICANT: Cart, Brian
TITLE OF INVENTION: AXMT-014, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods for Its Use
FILE REFERENCE: 045600/274143
CURRENT APPLICATION NUMBER: US/10/782,141
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: 60/448,632
PRIOR FILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 2019
TYPE: DNA
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2019)
US-10-782-141-2
Query Match 100.0%; Score 2019; DB 8; Length 2019;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGAAATATGATTTCTTATCAAAATACAAATGATATGAAATTTGATGTTCCCGG 60
Db 1 GTGAAATATGATTTCTTATCAAAATACAAATGATATGAAATTTGATGTTCCCGG 60
QY 61 AATTAACAATATGCAATGCAAGATATCTTTGCAAGGATCAATATATTTCCAT 120
Db 61 AATTAACAATATGCAATGCAAGATATCTTTGCAAGGATCAATATATTTCCAT 120
QY 121 AACCTGACGCTTGTGACGAGGACGATGCAAGATACGTGGATTCAGTTCGATATA 180
Db 121 AACCTGACGCTTGTGACGAGGACGATGCAAGATACGTGGATTCAGTTCGATATA 180
QY 181 GTAACTATGGGACATACCTTATACAAATTTCTGTAACCCGGTATAGTGAATTCCT 240
Db 181 GTAACTATGGGACATACCTTATACAAATTTCTGTAACCCGGTATAGTGAATTCCT 240

Db 181 GTAACATATGGGACATACCTTATACAAATCTCTGTAGAACCCGGTATAGGTGAAATTCCT 240
QY 241 GTAATATTTTCAATTAATAAACAACTCATTCGGCTTCTGCTAAATCTGTGGAGACATT 300
Db 241 GTATATTTTCAATTAATAAACAACTCATTCGGCTTCTGCTAAATCTGTGGAGACATT 300
QY 301 TCTATATGTGATTTAGATCTATTAATTCGTAAGAGGTAGACAGACGGTAAAGTAC 360
Db 301 TCTATATGTGATTTAGATCTATTAATTCGTAAGAGGTAGACAGACGGTAAAGTAC 360
QY 361 GGGGTTCAGATTTTGAAGGTGAATGACCTGCTTATCAGATTAATTAATCTTCAATCTT 420
Db 361 GGGGTTCAGATTTTGAAGGTGAATGACCTGCTTATCAGATTAATTAATCTTCAATCTT 420
QY 421 GAGATTTGCTTACAGTAAATCAATTCCTAAAACTTGTCTACAGATTAATTAATCTTCA 480
Db 421 GAGATTTGCTTACAGTAAATCAATTCCTAAAACTTGTCTACAGATTAATTAATCTTCA 480
QY 481 CAAGCACGGGAGAGAAATTTCACTAAAATTTTACAGAGGTCAATTAATCAAGACAGAAAGCT 540
Db 481 CAAGCACGGGAGAGAAATTTCACTAAAATTTTACAGAGGTCAATTAATCAAGACAGAAAGCT 540
QY 541 GAAATATATTAATTTGCTTACGTAATGTCGCAAGCTGCAATGCTATTAATTAATTAAG 600
Db 541 GAAATATATTAATTTGCTTACGTAATGTCGCAAGCTGCAATGCTATTAATTAATTAAG 600
QY 601 GACGAGTTAAATTAATAAAGAAATGGGACCTAGTGTCCACCGTTTATCCAGGGTCA 660
Db 601 GACGAGTTAAATTAATAAAGAAATGGGACCTAGTGTCCACCGTTTATCCAGGGTCA 660
QY 661 GGGAGAACTGATTTGTAAACGAGCGGTTAAAAGCGAAATAAAGAGTAACTAATTAATTTG 720
Db 661 GGGAGAACTGATTTGTAAACGAGCGGTTAAAAGCGAAATAAAGAGTAACTAATTAATTTG 720
QY 721 GTAGGTGTGTATTAACAAGGTTTATGATCAATTAAGACAGCGGGTACAGTGTCTGAAGT 780
Db 721 GTAGGTGTGTATTAACAAGGTTTATGATCAATTAAGACAGCGGGTACAGTGTCTGAAGT 780
QY 781 TGGTCCAAATTTTAAATTTTCTGTAAGAAATGACGTTGGCGGTTATGATTAATTTGCT 840
Db 781 TGGTCCAAATTTTAAATTTTCTGTAAGAAATGACGTTGGCGGTTATGATTAATTTGCT 840
QY 841 AATATTTCCAACTTATGATTTTGAATAATATCAATTAAGCAACAAGTGAAGTTAACTAG 900
Db 841 AATATTTCCAACTTATGATTTTGAATAATATCAATTAAGCAACAAGTGAAGTTAACTAG 900
QY 901 GAAATTTATACATTCAGTGGGATTTTCAGGGGAAATTAATGTTGGGAACGGTTTTT 960
Db 901 GAAATTTATACATTCAGTGGGATTTTCAGGGGAAATTAATGTTGGGAACGGTTTTT 960
QY 961 AGCTTTAATTCGGTAGAAGCAAAATGGAACAGGGGACCTTGTAGTTACTTGGCTTCAA 1020
Db 961 AGCTTTAATTCGGTAGAAGCAAAATGGAACAGGGGACCTTGTAGTTACTTGGCTTCAA 1020
QY 1021 GCTATAGATTAATTAATGATCAATTTCACTTGGTGTATCTTAAGTGGCTGAGG 1080
Db 1021 GCTATAGATTAATTAATGATCAATTTCACTTGGTGTATCTTAAGTGGCTGAGG 1080
QY 1081 GGAACCTGCTATTAATGAGCACTTCAACAAGGGTAAACGGTCTTTCAACCTATGCTCGA 1140
Db 1081 GGAACCTGCTATTAATGAGCACTTCAACAAGGGTAAACGGTCTTTCAACCTATGCTCGA 1140
QY 1141 ACTACAGTAAATTAATCAAGTAAATTAATTTTGGCAATTCGATTAATTAATTAATTAAT 1200
Db 1141 ACTACAGTAAATTAATCAAGTAAATTAATTTTGGCAATTCGATTAATTAATTAATTAAT 1200
QY 1201 TCAATTAAGTATGATTAATGCAATCAACCGTTTGTGGTATTAATTAATTAATTAATTAAT 1260
Db 1201 TCAATTAAGTATGATTAATGCAATCAACCGTTTGTGGTATTAATTAATTAATTAATTAAT 1260
QY 1261 TCACTGTGCAAAATTTTTCGACAACTAATTAATCTTCTGTATGAGGTAAACAGTTCT 1320
Db 1261 TCACTGTGCAAAATTTTTCGACAACTAATTAATCTTCTGTATGAGGTAAACAGTTCT 1320

QY 1321 GGGTACTCAGACAAATGGAATCTGTGTTACAGAGGATTAATTAAGGATCTACACCTACT 1380
Db 1321 GGGTACTCAGACAAATGGAATCTGTGTTACAGAGGATTAATTAAGGATCTACACCTACT 1380
QY 1381 CGTACAAATTAATCTCATAGATTTATCAAAATGGGAGATGTTCAAAATGAACCTTCAGA 1440
Db 1381 CGTACAAATTAATCTCATAGATTTATCAAAATGGGAGATGTTCAAAATGAACCTTCAGA 1440
QY 1441 GTTAACTGATTTGGTGGACATACATCAAGTATGAATAAAGATTAATCAATTAATCAAGAT 1500
Db 1441 GTTAACTGATTTGGTGGACATACATCAAGTATGAATAAAGATTAATCAATTAATCAAGAT 1500
QY 1501 AAAATTAAGCAAAATTCCTGACATTAAGGCTTTGGCTTACAGAGGATTAATTAATTAATGA 1560
Db 1501 AAAATTAAGCAAAATTCCTGACATTAAGGCTTTGGCTTACAGAGGATTAATTAATTAATGA 1560
QY 1561 GGAAGTTACGTACAGCTGGGCTGGTTATACAGAGAGAGATGATTAATTAATTAATTAAT 1620
Db 1561 GGAAGTTACGTACAGCTGGGCTGGTTATACAGAGAGAGATGATTAATTAATTAATTAAT 1620
QY 1621 CAAGCAAGTTTAAATTAATGATTTAACTTGTGACCCAGATTAATAATTAATTAATTAAT 1680
Db 1621 CAAGCAAGTTTAAATTAATGATTTAACTTGTGACCCAGATTAATAATTAATTAATTAAT 1680
QY 1681 CTTGCTACAGAGTGGAGGACCTGGTCCGTTCCGAGTAAAGATGCTGCGCAAGTTCT 1740
Db 1681 CTTGCTACAGAGTGGAGGACCTGGTCCGTTCCGAGTAAAGATGCTGCGCAAGTTCT 1740
QY 1741 GTTTCAAATGCTAAATTTTCTGTCAGCTACAGGTGCTATAGTTCAATTTATGATG 1800
Db 1741 GTTTCAAATGCTAAATTTTCTGTCAGCTACAGGTGCTATAGTTCAATTTATGATG 1800
QY 1801 GACACCTTAATGTTACATTAATTAATCAATTAATGATTAATTAATTAATTAATTAATTAAT 1860
Db 1801 GACACCTTAATGTTACATTAATTAATCAATTAATGATTAATTAATTAATTAATTAATTAAT 1860
QY 1861 GGTACCACTTAATGTTGACAAAGTGAATTTATCCCAATTAATTAATTAATTAATTAATTAAT 1920
Db 1861 GGTACCACTTAATGTTGACAAAGTGAATTTATCCCAATTAATTAATTAATTAATTAATTAAT 1920
QY 1921 TGTACGAATGCTCAATTCGAGAGAGACATATGATTAATTAATTAATTAATTAATTAATTAAT 1980
Db 1921 TGTACGAATGCTCAATTCGAGAGAGACATATGATTAATTAATTAATTAATTAATTAATTAAT 1980
QY 1981 AAAAAAAAAAGATTTGTAATAGTTTATTAATTAATTAATTAATTAATTAATTAATTAAT 2019
Db 1981 AAAAAAAAAAGATTTGTAATAGTTTATTAATTAATTAATTAATTAATTAATTAATTAAT 2019

RESULT 2
US-10-782-141-1
; Sequence 1, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargis, Tracy
; APPLICANT: Kozel, Michael G.
; APPLICANT: Duck, Michael B.
; TITLE OF INVENTION: Methods for its use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10782,141
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Faesteq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis


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; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carotzi, Nadine
; APPLICANT: Hargis, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/27413
; CURRENT APPLICATION NUMBER: US/10/782,141
; PRIOR APPLICATION NUMBER: 2004-02-20
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ. ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
US-10-782-141-4
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Query Match          99.6%; Score 2010; DB 8; Length 2010;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2010; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 10 ATGAAATCTTATCAAAATACAAATGAATATGAATTCGTGATGGTCCCGAAATTAACACA 69
DB 1 ATGAAATCTTATCAAAATACAAATGAATATGAATTCGTGATGGTCCCGAAATTAACACA 60
QY 70 AATATGCAACAGATATCTTTTGCAAGATCCAAATATATTTCTATTAACCTGGAC 129
DB 61 AATATGCAACAGATATCTTTTGCAAGATCCAAATATATTTCTATTAACCTGGAC 120
QY 130 GCTTGTCAGGGAAGGCGCATGGAATACGTGGGAATCAGTCCGATATATGTAATCTATT 189
DB 121 GCTTGTCAGGGAAGGCGCATGGAATACGTGGGAATCAGTCCGATATATGTAATCTATT 180
QY 190 GGAACATACCTTATACAAATCTTGCTAGAACCCGGATATAGTGAATTCCTGTATATTT 249
DB 181 GGAACATACCTTATACAAATCTTGCTAGAACCCGGATATAGTGAATTCCTGTATATTT 240
QY 250 TCATATATTAACAACATCATTTCCGTCTTCTGCTCAATCTGTGGCAGCATTTCTATATGT 309
DB 241 TCATATATTAACAACATCATTTCCGTCTTCTGCTCAATCTGTGGCAGCATTTCTATATGT 300
QY 310 GATTAGTATCTATTAATTCGTAAGAGGTAGACGAGAGCGGTTAATGTAAGGGGTTGCA 369
DB 301 GATTAGTATCTATTAATTCGTAAGAGGTAGACGAGAGCGGTTAATGTAAGGGGTTGCA 360
QY 370 GATTTTGAAGGTGAATGACTGCTTATCAAGATTAATTCCTATTAATCTTGAAGATTTG 429
DB 361 GATTTTGAAGGTGAATGACTGCTTATCAAGATTAATTCCTATTAATCTTGAAGATTTG 420
QY 430 CTATACAGATTAATTAATCTTAATAAACTTGCTGAGTATTAACGTTCCAAAGCAGG 489
DB 421 CTATACAGATTAATTAATCTTAATAAACTTGCTGAGTATTAACGTTCCAAAGCAGG 480
QY 490 GAAGAAGATTCCTAATACTTTAGAGGGGTCATTATCAAGACGAAAGCTGAATTTTA 549
DB 481 GAAGAAGATTCCTAATACTTTAGAGGGGTCATTATCAAGACGAAAGCTGAATTTTA 540
QY 550 TTAATGCTTAAGTATGCAAGCTCAAAATGTGCAATTAATTAATTAAGGAGCGAGTT 609
DB 541 TTAATGCTTAAGTATGCAAGCTCAAAATGTGCAATTAATTAATTAAGGAGCGAGTT 600
QY 610 AATATTAATAAAGAAATGGGAGCTATGTGTGCACCGTTGATCCAGGGTCAAGGAGAACT 669
DB 601 AATATTAATAAAGAAATGGGAGCTATGTGTGTGCACCGTTGATCCAGGGTCAAGGAGAACT 660
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QY 670 GATTTGAACGAGCGGTTAAAGCGAAATTAAGAGTATTAATTAATTTGTTAGGGTGG 729
DB 661 GATTTGAACGAGCGGTTAAAGCGAAATTAAGAGTATTAATTAATTTGTTAGGGTGG 720
QY 730 TATTAACAAGGTTTATAGATCAGATTAAGACAGCGGGTACAAAGTCTGAAGTTTGCGAAA 789
DB 721 TATTAACAAGGTTTATAGATCAGATTAAGACAGCGGGTACAAAGTCTGAAGTTTGCGAAA 780
QY 790 TTTAATAAATTTTCGTAGAGAAATGACGTTGGCGGTATTTGATATTTGCTATATTTCCA 849
DB 781 TTTAATAAATTTTCGTAGAGAAATGACGTTGGCGGTATTTGATATTTGCTATATTTCCA 840
QY 850 ACTTATGATTTTGAATAATATCCATTAGCAACAAGTATGATTTAATCTAGGAAATTTAT 909
DB 841 ACTTATGATTTTGAATAATATCCATTAGCAACAAGTATGATTTAATCTAGGAAATTTAT 900
QY 910 ACAGATCCAGTGGATATTCAGGGGAAATTAATGTTGGGAACGGTTTTTATGCTTTAAT 969
DB 901 ACAGATCCAGTGGATATTCAGGGGAAATTAATGTTGGGAACGGTTTTTATGCTTTAAT 960
QY 970 TCGGTAGAAAGCAAAATGGAACACGGGGAACCTGTTATGTTACTTGCTTACACTATAGT 1029
DB 961 TCGGTAGAAAGCAAAATGGAACACGGGGAACCTGTTATGTTACTTGCTTACACTATAGT 1020
QY 1030 ATATATAGTCATTTCTATTAATCTTCAGCTTGGTATCTTAGTGGCTGGGGGGAACCTCGT 1089
DB 1021 ATATATAGTCATTTCTATTAATCTTCAGCTTGGTATCTTAGTGGCTGGGGGGAACCTCGT 1080
QY 1090 CATTAAGAAGACTTCAAAAGGTTAACGGTGTCTTTTCAACGTATGCTGGAACCTAGAGT 1149
DB 1081 CATTAAGAAGACTTCAAAAGGTTAACGGTGTCTTTTCAACGTATGCTGGAACCTAGAGT 1140
QY 1150 AATTAATCCAGTATATTTATTTTGGCAATACCGATATTTTAAATATTTTCAATTAAGT 1209
DB 1141 AATTAATCCAGTATATTTATTTTGGCAATACCGATATTTTAAATATTTTCAATTAAGT 1200
QY 1210 AGATATGCAATCAACCGTTTGTGGGTATTCATTCGCCAGGCACTTGTTCACAGTGA 1269
DB 1201 AGATATGCAATGCAACCGTTTGTGGGTATTCATTCGCCAGGCACTTGTTCACAGTGA 1260
QY 1270 GAATTTTTTCGACAAACATTAATCTTCTGTATGAGGTAAACAGTCTGGGTACTCA 1329
DB 1261 GAATTTTTTCGACAAACATTAATCTTCTGTATGAGGTAAACAGTCTGGGTACTCA 1320
QY 1330 CAGACAAATGAATCTGTGTTACAGGTATTAATAGATCTACACTTATGTTGTAAT 1389
DB 1321 CAGACAAATGAATCTGTGTTACAGGTATTAATAGATCTACACTTATGTTGTAAT 1380
QY 1390 TACTCTCATAGATTAATCAATGCGGCACTGTTCAAAATGAACCTCCAGAGTTAACGTA 1449
DB 1381 TACTCTCATAGATTAATCAATGCGGCACTGTTCAAAATGAACCTCCAGAGTTAACGTA 1440
QY 1450 TTTGTTGACACATACAAAGTATGAATAAAGATTAATCGAATTTATCCAGATTAATTAAG 1509
DB 1441 TTTGTTGACACATACAAAGTATGAATAAAGATTAATCGAATTTATCCAGATTAATTAAG 1500
QY 1510 CAATTTCTGCAATTAACCTTTGCTCCCAAGAGGTATCAGATATGCAAGAGTTAC 1569
DB 1501 CAATTTCTGCAATTAACCTTTGCTCCCAAGAGGTATCAGATATGCAAGAGTTAC 1560
QY 1570 GTCAAGCTGGGCTGTGTATACAGAGGAGATGTATGTAACGTTACCTATCAAGCAAGT 1629
DB 1561 GTCAAGCTGGGCTGTGTATACAGAGGAGATGTATGTAACGTTACCTATCAAGCAAGT 1620
QY 1630 TTAATAAATACGTTTAACTTCTGACCCCAAGATTAATAATTAACGTTTGAACCTTCCCTAC 1689
DB 1621 TTAATAAATACGTTTAACTTCTGACCCCAAGATTAATAATTAACGTTTGAACCTTCCCTAC 1680
QY 1690 GCGAGTGAAGAGACCTGTGCTGTTCCGAGTATGAAGATGTGCGCAAGTTCTGTTCAAT 1749
DB 1681 GCGAGTGAAGAGACCTGTGCTGTTCCGAGTATGAAGATGTGCGCAAGTTCTGTTCAAT 1740
QY 1750 GCTAATTTTTCTCGTCAAGCTACAGGTGCTATAGTTCAATTTGATTAATGGAACACTTA 1809
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Db 1590 GGACCTCTCATGATGATTAATGCGGCATGTTGTATGATGAACTCCAGAGTTAC 1649
Qy 1447 GTATTGGTTGACACATGATGAAAAAGATAATTCGATTTATCGAGTAAATT 1506
Db 1650 GTATATGTTGAGACATACAGATTAAACGTGAAATATATGAAACCAATCAATT 1709
Qy 1507 ACGGAATTCCTGAGATGAAAGCTTTGGCTTACCAGAGATACAGATATGCGAGAGT 1566
Db 1710 ACACAAATACCGGCGGAGAGATATATTAATCTTCAAAATTAATCTTGTAAATGCTTATACC 1769
Qy 1567 TACGTACAGCTGGGCTT 1584
Db 1770 TATGTAAATAAGGCACT 1787

RESULT 6
US-10-781-979-4
Sequence 4, Application US/10781979
Publication No. US20040250311A1
GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine
APPLICANT: Hargies, Tracy
APPLICANT: Koziele, Michael G.
APPLICANT: Duck, Nicholas B.
APPLICANT: Carr, Brian
TITLE OF INVENTION: XM1-008, A Delta-Endotoxin Gene and
FILE OF INVENTION: Methods for its use
FILE REFERENCE: 045600/274147
CURRENT APPLICATION NUMBER: US/10/781,979
PRIOR FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: 60/448,797
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 2073
TYPE: DNA
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2073)
US-10-781-979-4

Query Match 36.6%; Score 739.8; DB 8; Length 2073;
Best Local Similarity 69.7%; Pred. No. 1.4e-163;
Matches 1135; Conservative 0; Mismatches 422; Indels 72; Gaps 7;

Qy 10 ATGAATCTTATCAAAATPACAAATGATGATGAAATTCGTGATGGTCCCGAATPACACA 69
Db 1 ATGAGTCCATATCAAAATPACAAATGATGATGAAATTCGTGATGGTCCCGAATPACACA 60
Qy 70 AATATGCAAAAGATATCTTTTGGCAAGGATCCAAATATATTTCTTATTAACCTGAGC 129
Db 61 AATAGCGCAAAAGATATCTTTTGGCAAGGATCCAAATATATTTCTTATTAACCTGAGC 120
Qy 130 GCTTGTGAGGAGGCGCATGCGAAGATACGTGGGAATCAGTCTCGAATATGATGAT 189
Db 121 GATGTGACAGGGAATCTCATGGGATGAAATTTGGGAATCAGCGAAGATPACAGATAT 180
Qy 190 GGGACATACCTTATACAAATCTTGTCTGAACCCGGTATAGTGGAAATTCCTGTAATTTT 249
Db 181 GGGATTAATCTTATAGAGTTGTATGAAACCTAGTTGGTGGAAATTAATACCTATTA 240
Qy 250 TCAATTAATAACAAACTATTCGCTCTTGTGTCATCTGTGGAGCACTTTCTATATGT 309
Db 241 TCAATTAATAAGAAATCTAATTCGATCTATGCTCAAACTGTGTGAGCACTTTCTATATGT 300
Qy 310 GATTATGATCTAATATTTGTAAGAGATGACAGAGCGGTGTAAGTGAAGGAGTTGCA 369
Db 301 GATTATTAATCTAATATTTGTAAGAGATGACAGAGCGGTGTAAGTGAAGGAGTTGCA 360
Qy 370 GATTGAGGAGTGAATGATGCTGTTATCAAGATTAATCTTCAATCTTGAAGATGG 429

Db 361 GATTTGAAGGTAAATGAAAAATTAATGACAGTATTAATCTTTATCTTTGGGCTTGG 420
Qy 430 CTTACAG-----ATTAATCAAAATCTTAAAAAACTGTGACGTAGTTAA 474
Db 421 CTTAAAGACGGTAACACATTTCAAAAGACAAATTAATCTGTATATGCGCAATGATTTAT 480
Qy 475 CAGTTCCAGACGGGAGAAAGATTTCACTTAATCTTTAGCAGGCTATTAATCAAGAC 534
Db 481 TATTTTAACTTTCCAGAAAGATTTCAATGAATTTAGAGAGGCTATGTCAGAAAC 540
Qy 535 AAAGCTGAAATATTAATTTATGCTAGTATGTCAGCTGCAATGTCATTTATTTCTA 594
Db 541 AATGCTCAAGTATTTGTTATTAATTTTACCTTCTTGGACACAGCTGCAATGTCATTTCTA 600
Qy 595 TTAAGGACGACGTTAAATTAATAAAGAAATGGGACCTAGTGTCCACCGTTTATCCA 654
Db 601 TTAAGGATGACGTTCAATTAATAAGCAATGTTCCATTTTGAAGTGCAGAAATGTA 660
Qy 655 GGGTCAGGAGAA-----CTGATTTGACAGCGG 684
Db 661 AGATCGGAATTAATATCACTTAACAGTGTGTGATTTTACCGGTGATTTACTATAGACGA 720
Qy 685 TTAAGACGAAATTAATAAGATATTAATTAATTTGTAGGCTGTTAACAAGGTTTA 744
Db 721 TTAATATGCAAAACGCGAGATATCAATTAATTTGTTATATGTTATGATAGTTTGA 780
Qy 745 GATCAGATTAAGACAGCGGCTACAGATGCTGAAGTTGTGCAAAATTAATTAATTTGCT 804
Db 781 AATAGATTAATAACGGGGGAGACAGGCTGCTGACACTTGCTGCAAAATTAATTAATTTGCT 840
Qy 805 AGAGAAATGACGTTGGCGATTTGATGATTAATTTGCTATTAATTTGCAACTTATGATTTGAA 864
Db 841 AGAGAAATGACGTTGGCGATTTGATGATTAATTTGCTATTAATTTGCAACTTATGATTTGAG 900
Qy 865 AATATTCATTAAGCAAAAGTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 924
Db 901 AATATTCATTTGCCAACAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 960
Qy 925 TATTCAGGGGAAATTTATGTTGGGAAACGGTTTT-----TTAGCTTAAATTCGGTGA 978
Db 961 TATTCATCGGGAATTAATTAATTTGTTATGATTAATTTGCTTAATTTGCTTAATTTGATG 1020
Qy 979 GCAATGGAACACGGGACCTGTTATGATTAATTTGCTTAATTTGCTTAATTTGATG 1038
Db 1021 GCTAATGGAACACGGGACCTGTTATGATTAATTTGCTTAATTTGCTTAATTTGATG 1080
Qy 1039 CATTCATTAATCTTACGCTTGTATCTTAATGCTGCGGGGGAATCTGCTATTAAG 1098
Db 1081 GAGTATGT-----TCGAGATATTTTCCGCGCTGGGTAGGAACTGCTCATTAAGAA 1131
Qy 1099 GACTTCAAAAGGTAACGGTGTCTTTCAAGTATGCTGGAACCTAGATTAATTTATCCA 1158
Db 1132 GACTACCAAAAGGTAACGGTATTTTCAACGATATGCTGGAACCTAGATTAATTTATCCA 1191
Qy 1159 GCTAATTAATTTTGGCAATACCGATATTAATTAATTTATTTCAATTAATTTGCTAATGCA 1218
Db 1192 GCTAATTAATTTTGGCAATACCGATATTAATTAATTTATTTCAATTAATTTGCTAATGCA 1248
Qy 1219 ATGCAACCGTTTGTGGGTATTCATATCCACCGCATCTTGTTCACCTGCAAGAAATTTT 1278
Db 1249 AACCTGTAAGAGATACCTGCTAGACAGAGATGCTGTATCAAAAGCAAGATTTTCT 1308
Qy 1279 CCGACAACACTTAATATCTTCTGTATGAGGTAAACAGTTCTGGG---TACTCAGACAGA 1335
Db 1309 AGGGTAGGGGACCTGATTTAAATTAATGATGACGATTAATATGGCTTAACAGAGATGCA 1368
Qy 1336 ATGGAATCTGTGTTACAGGATTAATTAAGAGATTAACACTTGTGCTAATAATTTACTCT 1395
Db 1369 ATGGAATCTAAGTCTTCCACTTGT-----ATTGCACTTAATGATGTTTAAAGACCTCT 1422
Qy 1396 CATAGATTAATCAATGAGGAGTGTCAAAATGAACCCGACAGATTAAGTATTTGCT 1455
Db 1423 CATAGATTAATCAATGAGGAGTGTGTATATGAAACCTCCAGAGTTAAGTATATGCT 1482

PRIOR FILING DATE: 1999-09-15
 : NUMBER OF SEQ ID NOS: 63
 : SOFTWARE: PatentIn version 3.2
 : SEQ ID NO 29
 : LENGTH: 2407
 : TYPE: DNA
 : ORGANISM: *Bacillus thuringiensis*
 US-10-428-961-29

Query Match 8.1%; Score 162.8; DB 6; Length 2407;
 Best Local Similarity 53.4%; Pred. No. 1.7e-27;
 Matches 434; Conservative 0; Mismatches 342; Indels 36; Gaps 3;

QY 161 GGGATCAGTCTCGGATATAGTAATCTATGGGACATACCTTATCAATCTTGGTAGAAC 220
 DB 158 GCGATGACGAAAAGAGCAGTATCTATGGACACACATGCTCTCTTATCACAGAC 217
 QY 221 CCGGATATAGTGAATCTCTGATATTTT-----CAATAATAACAACTCATTCCT 274
 DB 218 CTTCTCTTACTGATTAATTTCAATAGTATATGACCTTATAGTAAAGTACTAGAGTA 277
 QY 275 CTTCTGTCATCTGTGGACACCTTCTATATGATTTAGTATCTATATTTGCTAAAG 334
 DB 278 GTAGTGGACATTCATATCATATTTGTCTATATGACTTATATCTATTTTGAATTTAC 337
 QY 335 AGTATGACGAGCGGTGTTAAGTACGCGGTTGACATTTTGAAGGTAATGACTGCTT 394
 DB 338 GGGTATGACAGAGTTTAAATATGATGGATTCAGATTTTAAATGTTCTGACTCTTAT 397
 QY 395 ATCAAGATATATCTTC-----ATTATCTGAGATTTGGCTTACATA 439
 DB 398 ACAGAACTATTATAGAGCTCTGATAGCTGAATTAAGAACTTAAATCTGCTCTG 457
 QY 440 AATCAATCTTAAAAAATCTGCTGACGATGTTAAACAGTTCACAGCAGGAGAAAGATT 499
 DB 458 AAGAACTCCGACTCGTTTATGAATCCCGACCTAGATTTGATAGATTTTAAACCCGAG 517
 QY 500 TCACTAACTTTTACAGGCTCATTTATCAAGACAGAAAGCTGAATTTATTTATGCTTA 559
 DB 518 GGTCTTAAACGATATGCTGCTGTTAGTACAAATAGCCAAATATTTATTTACTT 577
 QY 560 CGTATGTCAGAGCTGCAATGTGATTTATTTATCTATTAAGGACCGCATTAATATATAA 619
 DB 578 CTTTGGAGCGCTGCAATTTTCCATTTATTTACTATCAAGGATGCTTACATAGATGACA 637
 QY 620 AAGATGGGACCTAGTGTGTCACCGTTGATCCAGGGTCAAGGAACTGATGTAGC 679
 DB 638 CTATTTGGGGCTATACATGCTACACCTTTTATA-----ATTATCAAT 682
 QY 680 AGCGTTTAAAGCGAAATTAAGAGATATCTAATTTATGTTAGGGTGTATTAACAGG 739
 DB 683 CAAAATAGTATAGACTTATGAACTATATATCTGATTTATGGGTATCATTTGGATATAGAG 742
 QY 740 GTTTAGATCAGATTAAGCAGCGGCTACAGTGTGAAGTTTGGTGCATTTATTAAT 799
 DB 743 GTTCAACCGAATTAAGCAACGAGGCTAGTGTCTAAGCTTGTGAATTTTCATGAT 802
 QY 800 TTGCTAGAGAAATGACCTTGGCGGTATTTGATATTTATTTGCTAATTTTCAACTATGAT 859
 DB 803 ATCGAGAGAGATACATTTATGAGATTTAAGAAATAGTACATCTTTTCAAGTTTATA 862
 QY 860 TTGAAAAATATCTTATGACCAAGTATAGATTTTATAGGAAATTTATATACATCAG 919
 DB 863 TTACTATTTACCCATATGAAAAAGATTTTCAAGTTGATAGGGTCAATTTATACATC 922
 QY 920 TGGGATATTCAGGGGAAATTTATGTTGGGAA 951
 DB 923 TTGGTTTGTACATGATGATGATCTTTAGGGGA 954

RESULT 9
 US-10-929-754-4
 ; Sequence 4, Application US/10929754

Publication No. US20050124803A1
 : GENERAL INFORMATION:
 : APPLICANT: ABDULLAH, MODH AMIR
 : APPLICANT: DEAN, DONALD H.
 : TITLE OF INVENTION: INSECTICIDAL CRYSTAL PROTEINS WITH ENHANCED TOXICITY
 : PUB REFERENCE: 22727/04179
 : CURRENT APPLICATION NUMBER: US/10/929,754
 : PRIOR FILING DATE: 2004-08-30
 : PRIOR APPLICATION NUMBER: 60/498,826
 : NUMBER OF SEQ ID NOS: 43
 : SOFTWARE: PatentIn Ver. 3.2
 : SEQ ID NO 4
 : LENGTH: 4391
 : TYPE: DNA
 : ORGANISM: *Bacillus thuringiensis*
 US-10-929-754-4

Query Match 6.6%; Score 133.6; DB 9; Length 4391;
 Best Local Similarity 48.1%; Pred. No. 1.8e-20;
 Matches 720; Conservative 0; Mismatches 704; Indels 74; Gaps 9;

QY 540 TGAATATTTATTTGCTACGTATGTCAGACGTGCAAAATGCGATTTATTTACTATTAG 599
 DB 1303 TGAATATTTATTTGCTGCTGCTATGACAAATTTGCAATCTGATTTACTTTTATACG 1362
 QY 600 GAGCGAGTTAAATATTAATAAGATGGGAGCTAGTGTCCACCGTTGATCCAGGGTCC 659
 DB 1363 GAGTCTCAATTTATGAGATTAATGTTGAGCGCACG-----AGCTAA 1407
 QY 660 AGGAGAACTGATTTGTAACAGCGGTTAAAGCGAAATTAAGATATCTAATTTATG 719
 DB 1408 TGCTCGATATATTTATTAACAAATTAACAATTAAGAAACAAAGAAATATACAGAAATTTG 1467
 QY 720 TGTAGGTGTATTAACAGGTTTATGATCGATTAAGCAGCGGGTCAAGTCTGAAT 779
 DB 1468 TATTAATTTGTTAAATTAAGGTTTAAATGATTTTAAACAGCAGCTCA----- 1516
 QY 780 TTGTCGAAATTTAATTAATTTGTCGAGAAATGACGTTGCGGTATTTGATTTATTC 839
 DB 1517 -TGGTAACTTTATATCTGTTATCTGATGAGAAATGACTCTTACTGATTAATTTATTC 1575
 QY 840 TATATTTCCACTATGATTTTGAATAATATCCATTAAGCAACAGTATAGTTAACTAG 899
 DB 1576 AATGTCCTATTTATTAAGCGAGATTAATATCTTACAGAAATTAACCGAATCACTAG 1635
 QY 900 GGAATTTATACGATTCAGTGGATTTTACGGGGGAAATTAATGTTGGACAGGTTTT 959
 DB 1636 GGAATTTATTCAGT---GTATTTAATGGGAGATATATGACTTATGACTCTTATTT 1692
 QY 960 TAGCTTAATTTGCTGTAAGCAATGGAACAGCGGGGCTGTTTGTGTTACTTGGCTTCA 1019
 DB 1693 TTTCTTTGAGAAAGCTGAATCACTTTATATACAGGACCCCATCTCTTCACTTGGCTAAA 1752
 QY 1020 AGCTATAGATATATATAGTCAATCTATTAATCTTCAAGCTTGTATTTAGTGGCTGGG 1079
 DB 1753 AGGATTTGATTTGTAACCAATTTCTATTTTATTTGAGACTTTTATCAGTGTCTAAA 1812
 QY 1080 GGGAACTCGCATTTATGAGACTTCAAAAGGTAACGTTGCTTTCAAGTATGCTGG 1139
 DB 1813 TAAGTATCTTATATCAATTAATTTCTAGTATTAACGAGGCTCTTTTATAGGGAACAGCAC 1872
 QY 1140 AACACAGATATATATCAAGTATATTTT-----GGCAATACGATATTTTAAAT 1196
 DB 1873 AGATTAATGAGGAGCTTTCTTACATTAATTTCAATTAATTTCAATTTATATATTT 1932
 QY 1197 TATTTCAATAGCTAGATATGCAATGCAACCGTTTGTGGTATCA---ATCCACGGCA 1253
 DB 1933 ATGACGGAATAATTAATATATATTTATCTTGGGGTATCTGTAATATTTACAAAAT 1992
 QY 1254 TCTTGTTCACGTCGAGATTTTTCGCAACACTAATAATCTTCTGATAGAGTTAA 1313
 DB 1993 GAATTTTCTGTAACAGATTAATATTTCTTCAAAAAGATTAATTAATGATGTCACAGAAC 2052

Qy	1314	CAGTTCGGGAGTACACAGACAAATGAAATCGTGTGACCGAGTAATTAATGAAGTCTACG	1373
Db	2053	GAAATTAACCTGTGTTCGGACAGATTTTGATTTTCTCACTAATTAAGAAGGAACTGAGTT	2112
Qy	1374	ACCTAGTCGTGACAAATTAATCTCATAGATTATCAAAATGCGGACGTGTTCMAAA-----	1427
Db	2113	AGCAAAATATTAATGATTATATCATATTTTATCTTATATCTTATATGTAATTAATGGGAAACGTT	2172
Qy	1428	---TGAAACCTCCAGAGTTAAACGTAATTTGGTGTGACATATCAAGTAATGAAAAAGATTA	1484
Db	2173	TGGTCAGAAAACGTCATGGTAATTTGGTTTGGCTTTTACACATAGTAAGTGTTCATCTAATTA	2232
Qy	1485	TCGAATTTATTCAGATTAATAATTAAGCAAAATTCCTGCAGTAAGAAAGCTTTTGCCTACACAG	1544
Db	2233	TACCATTTGCAGCGAATTAATAATTAACGCAAAATTCCTGTATGTGAAACCTTCGAGTTAATATG	2292
Qy	1545	AGGTACAGGATATGACAGAGGTTACGTCAACAGCTGGGCTCGTTATACAGAGAGAGATGT	1604
Db	2293	ATCGATTTCAATTAAGAAAAGGT-----CCGGATTTACGGGAGGAGATTT	2337
Qy	1605	AGTACGCTTACCTTATACAAGCAAGTTTAAATAATGCTTTAACTTTCGACACCCAGAAATTA	1664
Db	2338	GGTAAGAATGACAGCAAGATTCAGGTTTAACTATGCGTTTAAAGCTGAATTTAATTAAGATTA	2397
Qy	1665	AAATTTACCGTGTGTAGACTTCGCTACGCGAGTGAGAGACCTGTGCTCCGTTCCGAGTAGAAG	1724
Db	2398	AAATATGTGTGTGTGATAGTACGTTTAAATATGTAATCTAAGTTCTTAAATTAATTACTAGAAA	2457
Qy	1725	ATGG--TCGCAAGTTCGTGTTCAAAATGCTAAATTTTTCGTCCAGCTACAGGTGAGCTTA	1781
Db	2458	ATGGAAGAGGGGAAGGTAATATATACAAACAATAATTCACAAATATTTCTCCACATATGAGAG	2517
Qy	1782	TAGTTCATTTGATTATGTGACACCTTAAGTACTACATTTAATCAATCAGGTGTGAAT	1841
Db	2518	CTTTCTTATTTAAGTCTTTTACTATTAATCTACGACAGAAAATATATTTGATTTGACAAAT	2577
Qy	1842	AATTAATCAAAATCTATCTGTGTTCACACCTTATGTGTGACAAAGTCGAATTTATCCCAAT	1901
Db	2578	GGAGTAAACATTCGATATGTGTACACAGTTTGTGAAGATATACACTCTCTTATATTAAGA	2637
Qy	1902	TGACATCCAAATGAAAAATGTACGAAATGTCAATTTGAAAGAGACATATGTATGATGTGA	1961
Db	2638	TAAATATGAAATTCCTCCCACTAATGATACATTCACA-----GAAAAATATGA	2686
Qy	1962	AGGAGTCAATCTTGGAAACAAAAAAGAGATTGTAAATAGTTATTTATCAATTA	2019
Db	2687	CGAAATAATATGAATTAGAAGATCACAGAAACATTTAATATGTAATTTGTGATTTA	2744
RESULT 10			
US-10-428-961-5			
Sequence 5, Application US/10428961			
Publication No. US2003023711A1			
GENERAL INFORMATION:			
APPLICANT: Baum, James A.			
APPLICANT: Chu, Chih-Rel			
APPLICANT: Donovan, William P.			
APPLICANT: Gilmer, Mark J.			
APPLICANT: Ruper, Mark J.			
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin			
FILE REFERENCE: MECO201--1			
CURRENT APPLICATION NUMBER: US/10/428, 961			
PRIOR FILING DATE: 2003-05-02			
PRIOR APPLICATION NUMBER: 09/661,322			
PRIOR FILING DATE: 2000-09-13			
PRIOR APPLICATION NUMBER: 60/153,995			
PRIOR FILING DATE: 1999-09-15			
NUMBER OF SEQ ID NOS: 63			
SOFTWARE: PatentIn version 3.2			
SEQ ID NO 5			
LENGTH: 1959			

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; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-428-961-5

Query Match      5.9%; Score 119.8; DB 6; Length 1959;
Best Local Similarity 55.0%; Pred. No. 2.1e-17;
Matches 294; Conservative 0; Mismatches 217; Indels 24; Gaps 2

QY      435 AGATTAATCAATCCCTAAATAAATTCTGCGAGTAGTATTAAACAGTTCACAAGCGGGAGA 494
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      411 AGATPACCGGAATATGCAAGATCAAGAGCATTTATTTTGAGCGCTATGTTGCTTTAGA 470
QY      495 AGATTTCTACTAACTTTTACGAGGGGTCAATTATTCAGAAGAAAGCTGAAATTTATTAAT 554
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      471 ACTTGACATTTACTACTGCTATACCGCTTTTCAGAAATGAGAAAGTTCCATTAAT 530
QY      555 GCCTACGTATGTGCAAGCTGCAAAATGTGCATTTATTTACTATTAGGAGCGCAGTTAAATA 614
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      531 AATGTAAATATCTCAAGCTGCAAAATTTACACCTATTTATTTGAGAGACGCATCCCTTTT 590
QY      615 TAAAAAGAAATGGGGACAGTAGTGTCACCGTTGATCAAGGGTCAGGGAGAAACGATTTG 674
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      591 TGTATGTAAATGGGGGATGGCATCTTCCGATGTTAACCA-----TA 632
QY      675 TAACGAGCGGTAAAGAGCAAAATPAAAGATATCTAATTAATTTGTAAGGTGTATTA 734
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      633 TTACACAGGAACAATACATATATACAGAGGAATATTCTAACCATTTGCGTACATGATATA 692
QY      735 CAAGGGTTTATGATCATATTAAGACAGCGCGGTACAAAGTCTGAAGTTGGTGAATTTAA 794
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      693 TACAGGGCTTAATTAATTAATGA-----GGAGCAAAATCTGAAAGTTGGTGGTATTA 746
QY      795 TAAATTTGTAGAGAAATAGAGTTGGGGGTATTTGATATTTATTTGATATTTCCAACTTA 854
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      747 TCAATTCGGTAGAGCTTAAAGCTTAAAGGGGTATTAATTTAGTAGCCCTATTTCCAAAGCTA 806
QY      855 TGATTTTGAAAAATATCCATTAGCAACAAGTGTAGAGTTAACTAGAGAAATTTATATACAGA 914
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      807 TGATTACTGCACTTATCCATTCATATACAGATGCTCAGTTTACAAAGAAATTTATATACGA 866
QY      915 TCCAATGGGATTTTCAGGGGGAAATTAATGTGTGGGACGCGTTTTTACCTTAAT 969
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      867 TCCAATGGGAGAACAAATGCAACCTTCAGATTTGCAAGTACGAATGGTTTAAT 921

RESULT 11
US-10-782-020-4
; Sequence 4, Application US/10782020
; Publication No. US20040197916a1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782,020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1806
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1806)
US-10-782-020-4

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Db 1633 TTACTCATATAGGTATACAGTACCGTTTATGTATGATGCAAGTTTGTCTTAATCTGGG 1692
QY 1423 CAAATGAAACCTTCAGAGTTTACGTATTTGGTGGACACATACAGTATGAAAAAGAT 1482
Db 1693 ACCCTTATTTAAACAAGGTCATCTTTCTTGGACACATGCTATGCTGAAGAAC 1752
QY 1483 AATGATTTTTCAGATTAATTAATGCAAAATTCCTGCAAGTAAAGCTTTTCCCTACCA 1542
Db 1753 AATACATTTGATCAATTAATTAATGCAAAATTCCTGCAAGTAAAGCTTTTCCCTACCA 1812
QY 1543 GCAGGTAC 1550
Db 1813 TCAGGCAC 1820

RESULT 14

US-10-428-961-62
Sequence 62, Application US/10428961
Publication No. US20030237111A1
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rel
APPLICANT: Donovan, William P.
APPLICANT: Gilmer, Amy J.
APPLICANT: Ruper, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
FILE REFERENCE: NECO201-1
CURRENT APPLICATION NUMBER: US/10/428,961
PRIOR FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/661,322
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.2
SEQ ID NO 62
LENGTH: 3684
TYPE: DNA
ORGANISM: Bacillus thuringiensis
US-10-428-961-62

Query Match 5.8%; Score 116.8; DB 6; Length 3684;
Best Local Similarity 55.0%; Pred. No. 1.5e-16;
Matches 310; Conservative 0; Mismatches 227; Indels 27; Gaps 3;

QY 406 TATCTTCATATCTTGGAGATTGGCTTACAGATTAATCAATCTTAATAAACTTGTGAC 465
Db 400 TATCAACAGTCACCTTGAAGATGGCTAGAAAAACCGTATGATGCAAGAACGAGAGGTG 459
QY 466 GTAAGTAAACAGTTCCAGACCGGAGAGAGATTTCCTAACTTTAGCAGGTCATTA 525
Db 460 CTTTATCCCAATATATAGCTTAGAATGATTTCTTAATGAGATGCCGCTTTTGCA 519
QY 526 TCAAGACAGAAAGCTGAATATTTATTTATGCTTACGATGCAAGCTGCAAAATGTCAT 585
Db 520 ATTAGAAACCAAGAGTTCCATATATATG---GTATATGCTCAAGCTGCAAAATTTACAC 576
QY 586 TTTTATCTATTAAGGACGCAATTAATTAATAAAAGATGGGACCTAAGTGTCCACCG 645
Db 577 CTATTTATTTAGAGATGCTCTCTTTTGGTAGTAATTTGGGCTTACATCCCAAGAA 636
QY 646 TTTATTCAGAGGTTCAGGAGAACTGATTTTAAACGAGCGTTTAAAGCAAAATTAAGAG 705
Db 637 ATTCAAGC-----TTATTTAGAGCCCAAGTGAAGAAAAAGAGAA 678
QY 706 TATATCTAATTTATTTGAGGTGTATTAACAAGGTTTAAATCATGATTAAGACAGGCGGT 765
Db 679 TATTCGATTTATTTGCGCAAGATGATTAATACGGGTTTAAATTAATTTGAGA-----GGG 732
QY 766 ACAAGTCTGAAGTTTGGTGAATTTAATTAATTTGATGAGAAATGAGGTTGGCGGTA 825

Db 733 ACAATCTGAAGAGTGTTCGATATATATCAATTCCTGAGAGCTTAACGTAAGAGTA 792
QY 826 TTGGATATTTATTTCTAATTTTCCAACTTATGATTTTGAATAATTCATTAAGCAACAGT 885
Db 793 TTGATCTAGTGCACATTTCCCAAGCTATGACAGCGGTGTTTATCCAAATGAATACAGT 852
QY 886 GTAGAGTTAATCTAGGGAATTTATTAACATCCAGTGGATATTCAGGGGAAATTAATGT 945
Db 853 GCTCAATTTAACAAGAAATTTATTAACATCCATGATGGAGAACAAATGACCTTCAGGA 912
QY 946 TGGGAACGTTTTTAGCTTAAAT 969
Db 913 TTTCAGATACGAATTTGTTAAAT 936

RESULT 15

US-10-665-460A-7
Sequence 7, Application US/10665460A
Publication No. US20040096934A1
GENERAL INFORMATION:
APPLICANT: Freysinet, Georges
APPLICANT: Rang, Cecile
APPLICANT: Fritos, Roger
TITLE OF INVENTION: Peptide-sensitive modified Bacillus thuringiensis insecticidal
FILE REFERENCE: A35992-PCT-USA-A (072667.0191)
CURRENT APPLICATION NUMBER: US/10/665,460A
CURRENT FILING DATE: 2003-09-19
PRIOR APPLICATION NUMBER: PCT/FR02/00772
PRIOR FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: FR 01/03691
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 2019
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Artificial sequence description: Cry9Ca1 Glu-164
NAME/KEY: CDS
LOCATION: (1)..(2019)
US-10-665-460A-7

Query Match 5.6%; Score 113.4; DB 7; Length 2019;
Best Local Similarity 55.8%; Pred. No. 7e-16;
Matches 294; Conservative 0; Mismatches 206; Indels 27; Gaps 3;

QY 401 ATTATATCTTCAATATCTTGAAGATTGGCTTACAGATTAATCAATCTTAATAAACTTG 460
Db 440 ATGATATTAACAGTCTCCCTTCAAAATTTGGTGTATGTAATGATTAAGAAAATTTAA 499
QY 461 CTGACGTAGTTAAACGTTTCCAGACCGGAGAGAAATTTCACTTAACCTTTAGCGGGT 520
Db 500 GTGTTTGTGCTCAATTTATGCTTAGACCTTATTTGTTAATGCTATTCGA---T 556
QY 521 CATTATCAAGACAGAAAGCTGAATTTATTTATGCTTACGATGCAAGCTGCAAAATG 580
Db 557 TGTTCGAGTAATTTGACAGAGCTTCATTTACTGCTAGTATTTGACAGAGCTGTGAAT 616
QY 581 TGCATTTATCTAATTAAGGACGCAATTAATTAATAAAAGATGGGACCTAAGTGTGTC 640
Db 617 TACATTTGTTATTAATTAAGATGACATCTTTTGGAGAGAGATGGGATTTCA----- 670
QY 641 CACCGTTGATCCAGGTCAGGAGAACTGATTTTAAACAGCGGTTTAAAGCAAAATTA 700
Db 671 -----CACAGGGGAAATTTCAATTTATTAAGCTCAATTTGAACTTAACCG 718
QY 701 AAGATATCTAATTTATTTGAGGTGTATTAACAAGGTTTAAATGATTAAGACAGG 760
Db 719 CTAGATACATTAATTTCTGTAAGAACTTGTATTAATACAGTTTAAGTCTTTAAG----- 774

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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:54:29 ; Search time 189.099 Seconds
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Title: US-10-782-141-2

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Gapop 10.0 , Gapext 1.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	105	5.2	1860	7 US-11-058-727-15	Sequence 15, Appl
2	105	5.2	1860	7 US-11-108-389-15	Sequence 15, Appl
3	105	5.2	2010	7 US-11-058-727-11	Sequence 11, Appl
4	105	5.2	2010	7 US-11-108-389-11	Sequence 11, Appl
5	105	5.2	3621	7 US-11-058-727-1	Sequence 1, Appl
6	105	5.2	3621	7 US-11-108-389-1	Sequence 1, Appl
7	105	5.2	4874	7 US-11-058-727-17	Sequence 17, Appl
8	105	5.2	4874	7 US-11-108-389-17	Sequence 17, Appl
9	101.8	5.0	2019	7 US-11-058-727-55	Sequence 55, Appl
10	101.8	5.0	2019	7 US-11-058-727-87	Sequence 87, Appl
11	101.8	5.0	2019	7 US-11-108-389-55	Sequence 55, Appl
12	101.8	5.0	2019	7 US-11-108-389-87	Sequence 87, Appl
13	100.2	5.0	2019	7 US-11-058-727-59	Sequence 59, Appl
14	100.2	5.0	2019	7 US-11-058-727-91	Sequence 91, Appl
15	100.2	5.0	2019	7 US-11-108-389-59	Sequence 59, Appl
16	100.2	5.0	2019	7 US-11-108-389-91	Sequence 91, Appl
17	99.4	4.9	4359	9 US-11-031-643-3	Sequence 3, Appl
18	98.6	4.9	1863	7 US-11-058-727-19	Sequence 19, Appl
19	98.6	4.9	1863	7 US-11-108-389-19	Sequence 19, Appl
20	98.6	4.9	2019	7 US-11-058-727-57	Sequence 57, Appl
21	98.6	4.9	2019	7 US-11-058-727-89	Sequence 89, Appl
22	98.6	4.9	2019	7 US-11-108-389-57	Sequence 57, Appl
23	98.6	4.9	2019	7 US-11-108-389-89	Sequence 89, Appl

24	98.6	4.9	2022	7 US-11-058-727-7	Sequence 7, Appl
25	98.6	4.9	2022	7 US-11-058-727-21	Sequence 21, Appl
26	98.6	4.9	2022	7 US-11-058-727-25	Sequence 25, Appl
27	98.6	4.9	2022	7 US-11-058-727-29	Sequence 29, Appl
28	98.6	4.9	2022	7 US-11-058-727-33	Sequence 33, Appl
29	98.6	4.9	2022	7 US-11-058-727-43	Sequence 43, Appl
30	98.6	4.9	2022	7 US-11-058-727-49	Sequence 49, Appl
31	98.6	4.9	2022	7 US-11-058-727-67	Sequence 67, Appl
32	98.6	4.9	2022	7 US-11-058-727-69	Sequence 69, Appl
33	98.6	4.9	2022	7 US-11-058-727-75	Sequence 75, Appl
34	98.6	4.9	2022	7 US-11-058-727-81	Sequence 81, Appl
35	98.6	4.9	2022	7 US-11-108-389-7	Sequence 7, Appl
36	98.6	4.9	2022	7 US-11-108-389-21	Sequence 21, Appl
37	98.6	4.9	2022	7 US-11-108-389-25	Sequence 25, Appl
38	98.6	4.9	2022	7 US-11-108-389-29	Sequence 29, Appl
39	98.6	4.9	2022	7 US-11-108-389-33	Sequence 33, Appl
40	98.6	4.9	2022	7 US-11-108-389-43	Sequence 43, Appl
41	98.6	4.9	2022	7 US-11-108-389-49	Sequence 49, Appl
42	98.6	4.9	2022	7 US-11-108-389-67	Sequence 67, Appl
43	98.6	4.9	2022	7 US-11-108-389-69	Sequence 69, Appl
44	98.6	4.9	2022	7 US-11-108-389-75	Sequence 75, Appl
45	98.6	4.9	2022	7 US-11-108-389-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1

US-11-058-727-15
Sequence 15, Application US/11058727
Publication No. US20050261483A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flanagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnall
APPLICANT: James F. H. Wong
APPLICANT: Cao-Quo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
FILE REFERENCE: 35718/287809
CURRENT FILING DATE: 2005-02-15
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 1860
TYPE: DNA
ORGANISM: Bacillus thuringiensis (truncated)
FEATURE:
NAME/KEY: CDS
LOCATION: (10)...(1860)
FEATURE:
NAME/KEY: misc feature
LOCATION: (0)...(0)
OTHER INFORMATION: 49PVD
US-11-058-727-15

Query Match 5.2%, Score 105, DB 7, Length 1860;
Best Local Similarity 53.1%, Pred. No. 4.5e-16;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

GCACCTTCATATGATGATTTAGTATCTATATTCGTAAGAGGTAGACGAGCGGTGTA 354

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Db 205 GAAATTTTATGGAACAAGTAGAAGAACTCATTAATCAAAAATATAGAGAAATATGCAAG 264
QY 355 AGTGAAGGGGTTCACATTTTGGGGTGAATGACGCTTATTAAGATTATTTCTTCAT 414
Db 265 AATTAAGCGCTTTCGGAATTTAGAGATTAGTAAATTTTACCA---TTATATCTTACT 321
QY 415 TATCTTGAGATTGGCTTACAGATTAATCAATCTTAAAAAATTGCTGAGTAA 474
Db 322 GGGCTTGAGAAATGGGAAGAAAATCCAAATGTTCAAGACCTTAGAGATGTCGCAAT 381
QY 475 CAGTTCGAAGCAGCGGAAGAAATTCCTAACTTTAGACGGTTCATTAACAGACG 534
Db 382 CGATTTGAATCTCGATAGTTATTTATTCGCAATATATGCCA---TCTTTAGAGTAC 438
QY 535 AAAGCTGAATATTTATTTGCTAGTATGTCAGACGCTGCAATGCTTTATTACTA 594
Db 439 AATTTGAAGTACATTCCTACTGATATGCAATGCGCAACCTTCACTTACTGTTA 498
QY 595 TTAAAGGACGCACTTAATTAATAAAGAAATGGGGACTAGTGTCCACCGTTGTATCA 654
Db 499 TTAAAGGACGCGTCAATTTTGGAGAAATGGGGA-----TGTCA 540
QY 655 GGGTCAGGGAACCTGATTTGAACGACGGTTAAAGCGAAATTAAGATTAAT 714
Db 541 ACAACTACTATTAATTAATTAATGATCGTCAATGAACTTCTGAGATATTCGAT 600
QY 715 TATGTGTAGGGGTGATTAACAAGGGTTTATGATCAGATTAAGACGGGTTCAAGTGT 774
Db 601 CACTGTGTAAAGTGTATGAACCTGTTTACGAAATTTAAA-----GGCAGACGCT 654
QY 775 GAAGTTGTGCGAATTTTATAATTTTCTGAGAAATGACGTTGGCGGTATGATAT 834
Db 655 AAACATGGGTGACATTAACAATTCGTAAGAAATGACACTGGCGGTATTAGTGT 714
QY 835 ATTGCTATATTTCCAACTTATGATTTTGGAAAAATATCCATTAGCAACAGTGAAGTTA 894
Db 715 GTTGCAATTAATCCCAATTAATGACACGACGCTACCAATGAAAGCAACACTA 774
QY 895 ACTAGGGAATTTTATACAGATCCAGTGGG 923
Db 775 ACAAGGAAGTATTAACAGATCCACTGGG 803

RESULT 2
US-11-108-389-15
; Sequence 15, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Acetylcholinesterase
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1860
; TYPE: DNA
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; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10) ... (1860)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0) ... (0)
; OTHER INFORMATION: 49PVD
US-11-108-389-15

Query Match 5.2%; Score 105; DB 7; Length 1860;
Best Local Similarity 53.1%; Pred. No. 4.5e-16;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

QY 295 GCACCTTCTATATGATTTATGATATCAATTTCTGTAAGAGTGAAGAGCGGTGA 354
Db 205 GAAATTTTATGGAACAAGTAGAAGAACTCATTAATCAAAAATATAGAGAAATATGCAAG 264
QY 355 AGTGAAGGGGTTCACATTTTGGGGTGAATGACGCTTATTAAGATTATTTCTTCAT 414
Db 265 AATTAAGCGCTTTCGGAATTTAGAGATTAGTAAATTTTACCA---TTATATCTTACT 321
QY 415 TATCTTGAGATTGGCTTACAGATTAATCAATCTTAAAAAATTGCTGAGTAA 474
Db 322 GGGCTTGAGAAATGGGAAGAAAATCCAAATGTTCAAGACCTTAGAGATGTCGCAAT 381
QY 475 CAGTTCGAAGCAGCGGAAGAAATTCCTAACTTTAGACGGTTCATTAACAGACG 534
Db 382 CGATTTGAATCTCGATAGTTATTTATTCGCAATATATGCCA---TCTTTAGAGTAC 438
QY 535 AAAGCTGAATATTTATTTGCTAGTATGTCAGACGCTGCAATGCTTTATTACTA 594
Db 439 AATTTGAAGTACATTCCTACTGATATGCAATGCGCAACCTTCACTTACTGTTA 498
QY 595 TTAAAGGACGCACTTAATTAATAAAGAAATGGGGACTAGTGTCCACCGTTGTATCA 654
Db 499 TTAAAGGACGCGTCAATTTTGGAGAAATGGGGA-----TGTCA 540
QY 655 GGGTCAGGGAACCTGATTTGAACGACGGTTAAAGCGAAATTAAGATTAAT 714
Db 541 ACAACTACTATTAATTAATTAATGATCGTCAATGAACTTCTGAGATATTCGAT 600
QY 715 TATGTGTAGGGGTGATTAACAAGGGTTTATGATCAGATTAAGACGGGTTCAAGTGT 774
Db 601 CACTGTGTAAAGTGTATGAACCTGTTTACGAAATTTAAA-----GGCAGACGCT 654
QY 775 GAAGTTGTGCGAATTTTATAATTTTCTGAGAAATGACGTTGGCGGTATGATAT 834
Db 655 AAACATGGGTGACATTAACAATTCGTAAGAAATGACACTGGCGGTATTAGTGT 714
QY 835 ATTGCTATATTTCCAACTTATGATTTTGGAAAAATATCCATTAGCAACAGTGAAGTTA 894
Db 715 GTTGCAATTAATCCCAATTAATGACACGACGCTACCAATGAAAGCAACACTA 774
QY 895 ACTAGGGAATTTTATACAGATCCAGTGGG 923
Db 775 ACAAGGAAGTATTAACAGATCCACTGGG 803

RESULT 3
US-11-058-727-11
; Sequence 11, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
```

```

; TITLE OF INVENTION: Gene Encoding Proteins with Pesticidal
; FILE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 1218-1A
US-11-058-727-11

Query Match      5.2%; Score 105; DB 7; Length 2010;
Best Local Similarity 53.1%; Pred. No. 4.7e-16;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

QY 295 GCACTTTCTATATGATTTAGTATCTATATTTGTAAGAGGTAAGACGAGCGTGTGA 354
DB 337 GAATTTTATTTGGAACAGTAAGAACTCATTTATCAAAAATAGAGATATATGCAAG 396
QY 355 AGTACGGGGTTGCGAGATTTTGAAGGTAATGACGCTGATCAAGATTTATCTTCAT 414
DB 397 AATTAAAGCGCTTTGCAATTTAGAAAGATTAGTAAATATTAATCAAA--TTATATCTTACT 453
QY 415 TATCTTGAGATTTGGCTTACAGATTAATCAATCTTAAAACTTGTGACGTAGTTAAA 474
DB 454 GCGCTTGAAGATGGGAAGAAATCCAAATGTTCAAGAGCTTACAGAGATGTCCGAAT 513
QY 475 CAGTTCCAGACGCGGAAGAAATTTCACTTAACTTTTACGAGGTCATTTACAGACG 534
DB 514 CGATTTGAAATCCGTGATAGTTATTTACGCAATATATGCA--TCCTTTAGAGTGACA 570
QY 535 AAAGCTGAATATATTTATTTGCTACGATATGCAAGTGTCAATGTGCAATTTATCTA 594
DB 571 AATTTTGAAGTACCATTTCTTACTGTATATGCAATGCGACCAACTTCAATTTACTGTTA 630
QY 595 TTAAGGACGCAAGTTAATATTAATAAAGAAATGGGCACTAGTGTGCCACGTTGTATCA 654
DB 631 TTAAGGACGCGTCAATTTTGGAGAAATGGGGA-----TGGTCA 672
QY 655 GGGTCAGGAGCACTGATTTGTAACGACGGTTAAAGCCGAAATTAAGAGTATCTAAT 714
DB 673 ACAACTACTATTAATCTATTTATGATGTGCAAAATGAACTTACTGCAAGAAATTTCTGAT 732
QY 715 TATTTGTAGGGTGTGTAACAAGGGTTTGTAGTACATTAAGACAGGGGGTATCAAGTCT 774
DB 733 CACTGTGTAAGGTGATGTAAGAACTGTTTACCAAAATTAATAA-----GGCAGAGGCT 786
QY 775 GAAAGTTGTCGAATTTAATTAATTTTGTAGAGAAATGACGTTGGCGGTATTTGATAT 834
DB 787 AAACAATGGGTGCTATTAACCAATTCGTAGAGAAATGACACTGGCGGTTTATGATGTT 846
QY 835 AATGCTATTTTCAACTTATGATTTTGAAGAAATATCATTAAGAAAGATGATGATTA 894
DB 847 GTTGCAATTTATCCCAATTTATGACACACGACGTAACCAATGGAAGCAAAACCACTA 906
QY 895 ACTAGGAAATTTATACAGATCCAGTGGG 923
DB 907 ACAAGGGAAGTATATACAGATCCAGTGGG 935

```

```

RESULT 4
US-11-108-389-11
; Sequence 11, Application US/11108389
; Publication No. US20050261188A1.
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Gene Encoding Proteins with Pesticidal
; FILE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 1218-1A
US-11-108-389-11

Query Match      5.2%; Score 105; DB 7; Length 2010;
Best Local Similarity 53.1%; Pred. No. 4.7e-16;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

QY 295 GCACTTTCTATATGATTTAGTATCTATATTTGTAAGAGGTAAGACGAGCGTGTGA 354
DB 337 GAATTTTATTTGGAACAGTAAGAACTCATTTATCAAAAATAGAGATATATGCAAG 396
QY 355 AGTACGGGGTTGCGAGATTTTGAAGGTAATGACGCTGATCAAGATTTATCTTCAT 414
DB 397 AATTAAAGCGCTTTGCAATTTAGAAAGATTAGTAAATATTAATCAAA--TTATATCTTACT 453
QY 415 TATCTTGAGATTTGGCTTACAGATTAATCAATCTTAAAACTTGTGACGTAGTTAAA 474
DB 454 GCGCTTGAAGATGGGAAGAAATCCAAATGTTCAAGAGCTTACAGAGATGTCCGAAT 513
QY 475 CAGTTCCAGACGCGGAAGAAATTTCACTTAACTTTTACGAGGTCATTTACAGACG 534
DB 514 CGATTTGAAATCCGTGATAGTTATTTACGCAATATATGCA--TCCTTTAGAGTGACA 570
QY 535 AAAGCTGAATATATTTATTTGCTACGATATGCAAGTGTGCAATGTGCAATTTATCTA 594
DB 571 AATTTTGAAGTACCATTTCTTACTGTATATGCAATGCGACCAACTTCAATTTACTGTTA 630
QY 595 TTAAGGACGCAAGTTAATTAATAAAGAAATGGGCACTAGTGTGCCACGTTGTATCA 654
DB 631 TTAAGGACGCGTCAATTTTGGAGAAATGGGGA-----TGGTCA 672
QY 655 GGGTCAGGAGCACTGATTTGTAACGACGGTTAAAGCCGAAATTAAGAGTATCTAAT 714
DB 673 ACAACTACTATTAATCTATTTATGATGTGCAAAATGAACTTACTGCAAGAAATTTCTGAT 732

```

```

QY      475  CAGTTCACAGCAGGGGAAAGAATTTCTAACTTTTAGAGGGTCATTAACAAGCAG 553
Db      514  CGATTGGAATCCTGGATAGATTATTATTCAGCAATATATGCCA---TCTTTTAGGTGACA 570
QY      535  AAAGCTGAATATTTATTATTTGCCCTACGTATGTGCAGAGCTGCAGAAATGTGACTTTTACTA 594
Db      571  AATTTTGAAGTACACTTCCTTACTGTATATGTGAATGTGACAGCAACCTTCACTTTACTGTTA 630
QY      595  TTAAGGAGCGCAGTTAAATATATATAAAGAATGGGACCTAGTGTGCCACCGTGTATCCA 654
Db      631  TTTAAAGACCGCGTCATTTTGTGAGAAAGAATGGGGA-----TGGTCA 672
QY      655  GGGTCAGGGAGAACGTGATTGTACGAGGGGTTTAAAGCGAAATATAAAGATATTAAT 714
Db      673  ACAACTACTATTATTAATACTATTATATATGTGTCAATGAAACTTACTGCAGAAATTTTGAT 732
QY      715  TATTTGTATGGGTGTATATAACAAGGTTTATGATCAGATAGACAGCGGGGTACAGTGCT 774
Db      733  CACTGTGTAAAGTGGATGATAAATCGTGTTTAGAAAATTTAAA-----GGACAGAGGCT 786
QY      775  GAAAGTTTGGTCCAAATTTAATAATTTGTATAGAAAATGACGTTGGCGGTATTTGATATT 834
Db      787  AAACCAATGGGTGTGACTATATACCAATTCGTTAGAAAAGAACACATGGGGGTTTATGATGTT 846
QY      835  ATTTGCTAATTTTCCAACTATGATTTTGAAGAAATATTCATTAGCAACAAGTGTAGATT 894
Db      847  GTTGCACTATTATCCCAATATTTATACACAGCAGCAGTTCCTCAATGAAAGCAAGCACTA 906
QY      895  ACTAGGAAATTTATATACAGATCCAGTGGG 923
Db      907  ACAAGGGAAGTATATACAGATCCACTGGG 935

RESULT 6
US-11-108-389-1
/ Sequence 1, Application US/11108389
/ Publication No. US2005026118BA1
/ GENERAL INFORMATION:
/ APPLICANT: Andre R. Abad
/ APPLICANT: Ronald D. Flannagan
/ APPLICANT: Rafael Heitmann
/ APPLICANT: Theodore W. Kahn
/ APPLICANT: Albert L. Lu
/ APPLICANT: Billy Fred McCutchen
/ APPLICANT: James K. Presnail
/ APPLICANT: James F.H. Wong
/ APPLICANT: Cao-Guo Yu
/ TITLE OF INVENTION: Genes Encoding Proteins With Peestidal
/ TITLE OF INVENTION: Activity
/ FILE REFERENCE: 35718/291049
/ CURRENT APPLICATION NUMBER: US/11/108,389
/ PRIOR APPLICATION NUMBER: 60/391,786
/ PRIOR FILING DATE: 2002-06-26
/ PRIOR APPLICATION NUMBER: 60/460,787
/ PRIOR FILING DATE: 2003-04-04
/ PRIOR APPLICATION NUMBER: 10/606,320
/ PRIOR FILING DATE: 2003-06-25
/ NUMBER OF SEQ ID NOS: 134
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 3621
/ TYPE: DNA
/ ORGANISM: Bacillus thuringiensis
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1) ... (3621)
/ FEATURES:
/ NAME/KEY: misc_feature
/ LOCATION: (0) ... (0)
/ OTHER INFORMATION: C1Y1218-1
US-11-108-389-1

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QY	295	GCACTTCTATATGTGATTTAGATCTATATAATTCGTAAAGAGTACGAAAGCGTGTTA	354
Db	1067	GAATTTTATGGAACAAGTAGAAGAACTCATTATCAAAAATAATGCAAGATATGCAAGG	1126
QY	355	AGTACGCGGGGTGCAGATTTTGAAGGTGAATGACTGCTTATCAAGATTTATCTTCAT	414
Db	1127	AATTAAGCGCTTTCGGAATTAGAAGGATTTAGGTATATTAACAA---TTATATCTAACT	1183
QY	415	TATCTTGAGATTTGGCTTACAGATTAATTCAAATCTTAAAAAACTTGCTGACGTAGTTAA	474
Db	1184	GCGCTTGGAATAATGGGAAGAAATCCAAATGGTTCAAGAGCCTTACAGAGATGTCGAAT	1243
QY	475	CAGTTCCAACACGCGAAGAAGATTTCACTAAATCTTTAGACGGGTCATTTACAAACAG	534
Db	1244	CGATTTGAAATTCCTGGATAGTTATTTACCGCAATATATGCCA---TCTTTTAGAGTACA	1300
QY	535	AAAGCTGAAATATATTTATTATTCCTACGATATGTGCACGCTGCATAATGTGCATTTATCTA	594
Db	1301	AATTTTGAAATACCATTCCTTACTGTATATGCAATGGCAGCAACCTTCATTTACTGTTA	1366
QY	595	TTTAAGGACCGCAGTTAAATATTAATAAAGAAATGGGACCTAGTGTGCCACCGTTGATCCA	654
Db	1361	TTTAAAGACCGCTCAATTTTGGAGAAGAAATGGGGA-----TGGTCA	1402
QY	655	GGGTCAAGGAGAACTGATTTGTAACGACGCGTTTAAACGAAATATAAAGATATCTAAT	714
Db	1403	ACAACTACTATTTATATACATATATGATCGTCAAAATGAAACTTACTGCAAAATATTTGAT	1466
QY	715	TATGTGTAGAGGTGTATTAACAAGGTTTATGATCAGATTAAGACAGCGGGGTACAAAGTCT	774
Db	1463	CACGTGTATAAGTGTGTATGAAACGTGGTTTAGCAAAATTTAAAA-----GGCAGACGCT	1516
QY	775	GAAGTTTGTGTCCAAATTTAATAATTTCCGTAGAGAAATGACGTTGGCGGTATTTGATATT	834
Db	1517	AAACAATGGGTGTGACTATTAACCAATTCGTAGAAATAATGACATCGGCGGTTTATGATGTT	1576
QY	835	ATTGCTATATTTCCAACTTATGATTTTGAATAAATATCATTTAGCAACAGTGTAGAGTTA	894
Db	1577	GTTGCATATATTTCCCAATTTATGACACACGCACTGATCCCAATGGAAGAAAGCAACACTA	1636
QY	895	ACTAGGGAATTTATACAGATCCAGTGGG	923
Db	1637	ACAAAGGAAGTATATATACAGATCCACTGGG	1665

```
/ APPLICANT: Billy Fred McCutchen
/ APPLICANT: James K. Presnall
/ APPLICANT: James F. H. Wong
/ APPLICANT: Cao-Guo Yu
/ TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
/ FILE REFERENCE: 35718/291049
/ CURRENT APPLICATION NUMBER: US/11/108,389
/ PRIOR FILING DATE: 2005-04-18
/ PRIOR APPLICATION NUMBER: 60/391,786
/ PRIOR FILING DATE: 2002-06-26
/ PRIOR APPLICATION NUMBER: 60/460,787
/ PRIOR FILING DATE: 2003-04-04
/ PRIOR APPLICATION NUMBER: 10/606,320
/ PRIOR FILING DATE: 2003-06-25
/ NUMBER OF SEQ ID NOS: 134
/ SOFTWARE: FaestSeq for Windows Version 4.0
/ SEQ ID NO 17
/ LENGTH: 4874
/ TYPE: DNA
/ ORGANISM: Bacillus thuringiensis
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Genomic DNA 1218-1
US-11-108-389-17
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Query Match      5.2%; Score 105; DB 7; Length 4874;
Best Local Similarity 53.1%; Pred. No. 6,8e-16;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;
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QY 295 GCACCTTCATATGATGATTTAGTATCTATATTCGTAAGAAGAGGACGAGCGGTGTA 354
DB 1067 GAAATTTTATGGAACAAGAGGAAGAACTCATTTATCAAAAATAGCAGATATGCAAG 1126
QY 355 AGTACGGGGGTTGCAAGATTTTGAAGGTGAATGACTGCTTATCAAGATTTATCTTCAT 414
DB 1127 AATTAAGCGCTTCGGAATTAAGAAGATGATGATTAATATTAACCA---TATATCTTAAGT 1183
QY 415 TATCTTGAGATGCTGCTTACAGTAAATCAATCCCTTAATAAACTTGCTGACGTATTA 474
DB 1184 GCGCTTGAAGAAAGGAGAAATCCAAATGCTTCAAGACCTTACGAGATGCGCAAT 1243
QY 475 CAGTTCAGACGAGGAGAAAGATTCACCTAACTTTAGCAGAGGTCAATATCAAGACAG 534
DB 1244 CGATTTGAATCCTGATAGTTTATTTAGCAATATATGCA---TCTTTAGAGTGACA 1300
QY 535 AAAGTGAATATTTATTTATTTGCTACGATATGTCAGAGCTGCAATGTCAATTTACTA 594
DB 1301 AATTTTGAAGTACATTTCTTACTGATATGCAATGCGACGCAACCTTCATTTACTGTTA 1360
QY 595 TTAAGGAGCGCAATTAATTAATAAAGAAATGGGACATGATGTGCCACCGTTGTATCCA 654
DB 1361 TTAAGGAGCGCGTCAATTTTGGAGAAATGGGGA-----TGGTCA 1402
QY 655 GGGTCAGGAGCACTGATTTGTAACGAGCGGTAAAGCGAAATTAAGATTAATTAAT 714
DB 1403 ACACTACTATTTAATTAATCTTTATGATCGTCAATGAACTTCTGCAAGATATTTCTGAT 1462
QY 715 TATTTGTAGGCGGTGTAATAAAGGTTTATGATCAGATTAAGACGCGGTTACAGTGTCT 774
DB 1463 CACTGTGTAAAGTGTATGAAACGTGGTTAGCAAAATTTAAA-----GGCAGAGCGCT 1516
QY 775 GAAGTTTGGTCGAAATTTAATAATTTCTGATGAGAAATGACGTTGGCGGTATTTGATTT 834
DB 1517 AAACAATGGGTGATCATTAACCAATTCCTGAGAAATGACACCTGGCGGTTTATGATGTT 1576
QY 835 ATTGCTATATTTCCACTTATGATTTTGAAAAATATCATTAAGCAACAGTGTAGATTA 894
DB 1577 GTTGCAATATTTCCCAATTTATGACACGACGTAACCAATGAAAGCAACACTA 1636
QY 895 ACTAGGAAATTTTATACAGATCCAGTGGG 923
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DB 1637 ACAAGGAAATATATACAGATCCACTGGG 1665

RESULT 9

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US-11-058-727-55
/ Sequence 55, Application US/11058727
/ Publication No. US20050261483A1
/ GENERAL INFORMATION:
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/ APPLICANT: Andre R. Abad
/ APPLICANT: Ronald D. Flannagan
/ APPLICANT: Rafael Herrmann
/ APPLICANT: Theodore W. Kahn
/ APPLICANT: Albert L. Lu
/ APPLICANT: Billy Fred McCutchen
/ APPLICANT: James K. Presnall
/ APPLICANT: James F. H. Wong
/ APPLICANT: Cao-Guo Yu
/ TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
/ FILE REFERENCE: 35718/287809
/ CURRENT APPLICATION NUMBER: US/11/058,727
/ PRIOR FILING DATE: 2005-02-15
/ PRIOR APPLICATION NUMBER: 60/391,786
/ PRIOR FILING DATE: 2002-06-26
/ PRIOR APPLICATION NUMBER: 60/460,787
/ PRIOR FILING DATE: 2003-04-04
/ PRIOR APPLICATION NUMBER: 10/606,320
/ PRIOR FILING DATE: 2003-06-25
/ NUMBER OF SEQ ID NOS: 134
/ SOFTWARE: FaestSeq for Windows Version 4.0
/ SEQ ID NO 55
/ LENGTH: 2019
/ TYPE: DNA
/ ORGANISM: Bacillus thuringiensis (mutated)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(2019)
US-11-058-727-55
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```
Query Match      5.0%; Score 101.8; DB 7; Length 2019;
Best Local Similarity 58.6%; Pred. No. 2.8e-15;
Matches 228; Conservative 0; Mismatches 137; Indels 24; Gaps 2;
```

```
QY 535 AAAGTGAATATTTATTTATTTGCTTACGATATGCAAGCGCAAAATGTCATTTACTA 594
DB 583 AATTTTGAAGTACATTTCTTACTGATATGCAATGGACGCAACCTTCATTTACTGTTA 642
QY 595 TTAAGGAGCGCAATTAATTAATAAAGAAATGGGACATGATGTGTCCACCGTTGTATCCA 654
DB 643 TTAAGGAGCGCGTCAATTTTGGAGAAATGGGGA-----TGGTCA 684
```

```
QY 655 GGGTCAGGAGCACTGATTTGTAACGAGCGGTAAAGCGAAATTAAGATTAATTAAT 714
DB 685 ACACTACTATTTAATTAATTAATGATGATGTCMAATGAAACTTACGCAAAATATTTCTGAT 744
QY 715 TATTTGTAGGCGGTGTAATAAAGGTTTATGATCAGATTAAGCAGCGGTTACAGTGTCT 774
DB 745 CACTGTGTAAAGTGTATGAAACGTGGTTAGCAAAATTTAAA-----GGCAGAGCGCT 798
```

```
QY 775 GAAGTTTGGTCGAAATTTAATAATTTCTGATGAGAAATGACGTTGGCGGTATTTGATTT 834
DB 799 AAACAATGGGTGATCATTAACCAATTCCTGAGAAATGACACCTGGCGGTTTATGATGTT 858
QY 835 ATTGCTATATTTCCACTTATGATTTTGAAAAATATTCATTAAGCAACAGTGTAGATTA 894
DB 859 GTTGCAATATTTCCCAATTTATGACACGACGTAACCAATGAAAGCAACACTA 918
```

```
QY 895 ACTAGGAAATTTTATACAGATCCAGTGGG 923
DB 919 ACAAGGAAATATTAACAGATCCACTGGG 947
```

RESULT 10

US-11-058-727-87
; Sequence 87, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Prenail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: *Bacillus thuringiensis* (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-11-058-727-87

Query Match 5.0%; Score 101.8; DB 7; Length 2019;

Best Local Similarity 58.6%; Pred. No. 2.8e-15;
Matches 228; Conservative 0; Mismatches 137; Indels 24; Gaps 2;

```
QY 535 AAAGCTGAATATATTATTGCTTACGTATGTCGCAAGCTGCAATGTGCAATTATCTA 594
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 583 AATTGTGAAGTACATTCCTTACGTATATGCAATGCGACCAACTTCACTTTACTGTA 642
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 595 TTAAAGGAGCGCACTTAATATATATATATATATATATATATATATATATATATAT 654
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 643 TTAAAGGAGCGCGCAATTTTGGAGAAATGGGGA-----TGGTCA 684
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 655 GGGTCAGGAGAACTGATTTGTAACGAGCGGTTAAACGAAATATATATATATATAT 714
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 685 ACAACTACTATTTATATATATATATATATATATATATATATATATATATATAT 744
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 715 TATTGTGAGGGTGTGTATTAACAAGGTTTAGATCAGATTAAGACAGCGGGGTACAAGTCT 774
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 745 CACTGTGTAAAGTGTATGAACTGTTTAGCAAAATTTAAA-----GGCAGAGCGCT 798
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 775 GAAGTTTGTGCAATTTAATTAATTTTGTAGAGAAATGACGTTGGCGGTATTTGATATT 834
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 799 AAACAATGGGTTGACTATTAACCAATTCGTAAGAAATGACACTGGCGGTTTAGATGTT 858
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 835 ATTGCTATATTTCCAACTTATGATTTGAAAATATATCCATTAGACAAGTGTAGATTA 894
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 859 GTTGCAATTATTTCCCAATTTATGACACAATTAACGTATACCAATAGAAAGCAACAATA 918
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 895 ACTAGGAAATTTATACAGATCCAGTGGG 923
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 919 ACAAGGAAATATATACAGATCCAGTGGG 947
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 11
US-11-108-389-55
; Sequence 55, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:

APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Prenail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: *Bacillus thuringiensis* (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-11-108-389-55

Query Match 5.0%; Score 101.8; DB 7; Length 2019;
Best Local Similarity 58.6%; Pred. No. 2.8e-15;
Matches 228; Conservative 0; Mismatches 137; Indels 24; Gaps 2;

```
QY 535 AAAGCTGAATATATTATTGCTTACGTATGTCGCAAGCTGCAATGTGCAATTATCTA 594
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 583 AATTGTGAAGTACATTCCTTACGTATATGCAATGCGACCAACTTCACTTTACTGTA 642
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 595 TTAAAGGAGCGCACTTAATATATATATATATATATATATATATATATATATATATAT 654
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 643 TTAAAGGAGCGCGCAATTTTGGAGAAATGGGGA-----TGGTCA 684
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 655 GGGTCAGGAGAACTGATTTGTAACGAGCGGTTAAACGAAATATATATATATATATAT 714
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 685 ACAACTACTATTTATATATATATATATATATATATATATATATATATATATATAT 744
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 715 TATTGTGAGGGTGTGTATTAACAAGGTTTAGATCAGATTAAGACAGCGGGGTACAAGTCT 774
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 745 CACTGTGTAAAGTGTATGAACTGTTTAGCAAAATTTAAA-----GGCAGAGCGCT 798
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 775 GAAGTTTGTGCAATTTAATTAATTTTGTAGAGAAATGACGTTGGCGGTATTTGATATT 834
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 799 AAACAATGGGTTGACTATTAACCAATTCGTAAGAAATGACACTGGCGGTTTAGATGTT 858
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 835 ATTGCTATATTTCCAACTTATGATTTGAAAATATATCCATTAGACAAGTGTAGATTA 894
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 859 GTTGCAATTATTTCCCAATTTATGACACAATTAACGTATACCAATAGAAAGCAACAATA 918
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 895 ACTAGGAAATTTATACAGATCCAGTGGG 923
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 919 ACAAGGAAATATATACAGATCCAGTGGG 947
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 12
US-11-108-389-87
; Sequence 87, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn

```

; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-11-108-389-87
```

```

Query Match          5.0%; Score 101.8; DB 7; Length 2019;
Best Local Similarity 58.6%; Pred. No. 2,8e-15;
Matches 228; Conservative 0; Mismatches 137; Indels 24; Gaps 2;
```

```

QY 535 AAAGCTGAATATATATATATGCTAGTATGTCAGAGCTGCAGAAATGCAATTATTAACTA 594
    |||||
DB 583 AATTTTGAAGTACCATTTCTTACTGTATATGCAATGCGACCACTTATTTACTGTTA 642
    |||||
QY 595 TTAAGGAGCGCACTTAATATATATATATATGAGGAGCTAGTGTCTCCAGCTTGTATCA 654
    |||||
DB 643 TTAAGGAGCGCGTCAATTTTGGAGAGAAATGGGA-----TGTCA 684
    |||||
QY 655 GGGTCAGGAGAACTGATTTGTAACGAGCGGTTAAAGCGAAATTAAGATTAAT 714
    |||||
DB 685 ACAACTACTATATATATATATATATATATATATATATATATATATATATAT 744
    |||||
QY 715 TATGTGTAGGGGTATATACAAAGGTTTATGATCAGATTAAGACGGGGTAAATGCT 774
    |||||
DB 745 CACTGTATTAAGTGTATGATACTGGTTTACAAATTTAAA-----GGCAGAGCGCT 798
    |||||
QY 775 GAAGTTTGTGCAATTTATATATATATATATATATATATATATATATATATAT 834
    |||||
DB 799 AAACATGGGTTGACATATACCAATTCCTAGAGAAATGACATGGCGGTTTATGATGT 858
    |||||
QY 835 ATTGCTATATTTTCAACTTATGATTTTGAATAATATATCATTAGCAACAAGTGAAGTTA 894
    |||||
DB 859 GTTGCAATTTTCCCAATTTATGACAAATTAACGTACCAATAGAAAGCAACAACCTA 918
    |||||
QY 895 ACTAGGGAATTTATATACAGATCCAGTGGG 923
    |||||
DB 919 ACAAGGAAGTATATACAGATCACTGGG 947
    |||||
```

```

RESULT 13
US-11-058-727-59
; Sequence 59, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
```

```

; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-11-058-727-59
```

```

Query Match          5.0%; Score 100.2; DB 7; Length 2019;
Best Local Similarity 58.4%; Pred. No. 6,8e-15;
Matches 227; Conservative 0; Mismatches 138; Indels 24; Gaps 2;
```

```

QY 535 AAAGCTGAATATATATATGCTAGTATGTCAGAGCTGCAGAAATGCAATTATTAACTA 594
    |||||
DB 583 AATTTTGAAGTACCATTTCTTACTGTATATGCAATGCGACCACTTATTTACTGTTA 642
    |||||
QY 595 TTAAGGAGCGCACTTAATATATATATATATATGAGGAGCTAGTGTCTCCAGCTTGTATCA 654
    |||||
DB 643 TTAAGGAGCGCTCAATTTTGGAGAGAAATGGGA-----TGTCA 684
    |||||
QY 655 GGGTCAGGAGAACTGATTTGTAACGAGCGGTTAAAGCGAAATTAAGATTAAT 714
    |||||
DB 685 ACAACTACTATATATATATATATATATATATATATATATATATATATAT 744
    |||||
QY 715 TATGTGTAGGGGTATATACAAAGGTTTATGATCAGATTAAGACGGCGGTTACAAAGTCT 774
    |||||
DB 745 CACTGTATTAAGTGTATGATACTGGTTTACAAATTTAAA-----GGCAGAGCGCT 798
    |||||
QY 775 GAAGTTTGTGCAATTTATATATATATATATATATATATATATATATATATAT 834
    |||||
DB 799 AAACATGGGTTGACATATACCAATTCCTAGAGAAATGACATGGCGGTTTATGATGT 858
    |||||
QY 835 ATTGCTATATTTTCAACTTATGATTTTGAATAATATATCATTAGCAACAAGTGAAGTTA 894
    |||||
DB 859 GTTGCAATTTTCCCAATTTATGACAAATTAACGTACCAATAGAAAGCAACAACCTA 918
    |||||
QY 895 ACTAGGGAATTTATATACAGATCCAGTGGG 923
    |||||
DB 919 ACAAGGAAGTATATACAGATCACTGGG 947
    |||||
```

```

RESULT 14
US-11-058-727-91
; Sequence 91, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: Cao-Guo Yu
; APPLICANT: James F.H. Wong
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
```

CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 91
LENGTH: 2019
TYPE: DNA
ORGANISM: Bacillus thuringiensis (mutated)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2019)
US-11-058-727-91

Query Match 5.0%; Score 100.2; DB 7; Length 2019;
Best Local Similarity 58.4%; Pred. No. 6.8e-15;
Matches 227; Conservative 0; Mismatches 138; Indels 24; Gaps 2;

QY 535 AAAGCTGAATATATATATATGCTTACGATATGCAAGCTGCAATATGCAATTTATTTACTA 594
DB 583 AATTTGAAGTACCATTCCTTACTGTATATGCAATGCAAGCAACCTTCAATTTACTGTTA 642
QY 595 TTAAGGAGCGCAGTTAAATATTAATAAAGAAATGGGAGCTAGTGTGTCACCGTTGTATCCA 654
DB 643 TTAAGGAGCGCGTCAATTTTGGAGAAATGGGGA-----TGGTCA 684
QY 655 GGGTCAGGGAGAACTGATTTGTAACGAGCGGTTAAACGAAATTAAGAATATTTACTAAT 714
DB 685 ACAACTACTATTTATTAATCTATATATGATGTCGCAATGAACTTACTGAGATATTTGAT 744
QY 715 TATTGTAGGAGTGTATTAACAAGGTTTATGATCAATAAGACAGCGGGTATCAAGTGT 774
DB 745 CACTGTGTAAAGTGTATGAACTGTTTACCAAAATTAATA-----GGCAGAGCGCT 798
QY 775 GAAGTTGTGCGAATTTAATAATTTGTAAGAAATGACGTTGGCGGTATTTGATATTT 834
DB 799 AAACATAGGTTGATCTTAACCAATTCCTGAGAAATGACACTGGCGGTTTATGATGTT 858
QY 835 ATTGCTATATTTTCCAACTTATGATTTTGAATAATATCCATTAGCAACAGTGTAGATTA 894
DB 859 GTTGCAATATTTCCCAATTAATGACAAATACGTAACCAATGGAAGAAAGACAACTA 918
QY 895 ACTAGGAAATTTATACAGATCCAGTGGG 923
DB 919 ACAAGGGAAGTATATACAGATCCAGTGGG 947

RESULT 15

US-11-108-389-59
Sequence 59, Application US/11/108389
Publication No. US20050261188A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flanagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnall
APPLICANT: James F. H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
FILE REFERENCE: 35718/291049
CURRENT APPLICATION NUMBER: US/11/108,389
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26

PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 59
LENGTH: 2019
TYPE: DNA
ORGANISM: Bacillus thuringiensis (mutated)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2019)
US-11-108-389-59

Query Match 5.0%; Score 100.2; DB 7; Length 2019;
Best Local Similarity 58.4%; Pred. No. 6.8e-15;
Matches 227; Conservative 0; Mismatches 138; Indels 24; Gaps 2;

QY 535 AAAGCTGAATATATATATGCTTACGATATGCAAGCTGCAATATGCAATTTATTTACTA 594
DB 583 AATTTGAAGTACCATTCCTTACTGTATATGCAATGCAAGCAACCTTCAATTTACTGTTA 642
QY 595 TTAAGGAGCGCAGTTAAATATTAATAAAGAAATGGGAGCTAGTGTGTCACCGTTGTATCCA 654
DB 643 TTAAGGAGCGCGTCAATTTTGGAGAAATGGGGA-----TGGTCA 684
QY 655 GGGTCAGGGAGAACTGATTTGTAACGAGCGGTTAAACGAAATTAAGAATATTTACTAAT 714
DB 685 ACAACTACTATTTATTAATCTATATATGATGTCGCAATGAACTTACTGAGATATTTGAT 744
QY 715 TATTGTAGGAGTGTATTAACAAGGTTTATGATCAATAAGACAGCGGGTATCAAGTGT 774
DB 745 CACTGTGTAAAGTGTATGAACTGTTTACCAAAATTAATA-----GGCAGAGCGCT 798
QY 775 GAAGTTGTGCGAATTTAATAATTTGTAAGAAATGACGTTGGCGGTATTTGATATTT 834
DB 799 AAACATAGGTTGATCTTAACCAATTCCTGAGAAATGACACTGGCGGTTTATGATGTT 858
QY 835 ATTGCTATATTTTCCAACTTATGATTTTGAATAATATCCATTAGCAACAGTGTAGATTA 894
DB 859 GTTGCAATATTTCCCAATTAATGACAAATACGTAACCAATGGAAGAAAGACAACTA 918
QY 895 ACTAGGAAATTTATACAGATCCAGTGGG 923
DB 919 ACAAGGGAAGTATATACAGATCCAGTGGG 947

Search completed: December 19, 2005, 13:47:56
Job time: 194.099 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:27:04 ; Search time 251.648 Seconds

(without alignments)
14261.593 Million cell updates/sec

Title: US-10-782-141-2

Perfect score: 2019
Sequence: 1 gtgaaaaatgtaattctta.....atagttatttaccattaa 2019

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 segs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/ptodaca/1/ina/1_COMB.seq:*
- 2: /cgn2_6/ptodaca/1/ina/5_COMB.seq:*
- 3: /cgn2_6/ptodaca/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodaca/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodaca/1/ina/H_COMB.seq:*
- 6: /cgn2_6/ptodaca/1/ina/PCBUS_COMB.seq:*
- 7: /cgn2_6/ptodaca/1/ina/PP_COMB.seq:*
- 8: /cgn2_6/ptodaca/1/ina/RE_COMB.seq:*
- 9: /cgn2_6/ptodaca/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172.4	8.5	3468	US-09-001-982-9	Sequence 9, Appl1
2	172.4	8.5	3468	US-09-668-650-9	Sequence 9, Appl1
3	172.4	8.5	3471	US-09-002-285-71	Sequence 71, Appl1
4	172.4	8.5	3471	US-09-589-477-71	Sequence 71, Appl1
5	172.4	8.5	3471	US-10-099-285A-71	Sequence 71, Appl1
6	172.4	8.5	3726	US-09-001-982-11	Sequence 11, Appl1
7	172.4	8.5	3726	US-09-668-650-11	Sequence 11, Appl1
8	162.8	8.1	2407	US-09-661-322A-29	Sequence 29, Appl1
9	119.8	5.9	1959	US-09-661-322A-5	Sequence 5, Appl1
10	118.2	5.9	3934	US-08-100-709-3	Sequence 3, Appl1
11	118.2	5.9	3934	US-08-176-865-3	Sequence 3, Appl1
12	118.2	5.9	3934	US-08-474-038-3	Sequence 3, Appl1
13	118.2	5.9	3934	US-08-779-046-3	Sequence 3, Appl1
14	118.2	5.9	3934	US-08-881-340-3	Sequence 3, Appl1
15	116.8	5.8	3684	US-08-448-170-7	Sequence 7, Appl1
16	116.8	5.8	3684	US-08-961-803-5	Sequence 5, Appl1
17	116.8	5.8	3684	US-09-661-322A-62	Sequence 62, Appl1
18	112.4	5.6	4173	US-09-661-322A-37	Sequence 37, Appl1
19	111.8	5.5	1897	US-08-363-970-5	Sequence 5, Appl1
20	111.8	5.5	3471	US-09-002-285-73	Sequence 73, Appl1
21	111.8	5.5	3471	US-09-589-477-73	Sequence 73, Appl1
22	111.8	5.5	3471	US-09-661-322A-27	Sequence 27, Appl1
23	111.8	5.5	3471	US-10-099-285A-73	Sequence 73, Appl1
24	111.8	5.5	4344	US-08-532-547-4	Sequence 4, Appl1

25	111.8	5.5	4344	2	US-08-379-656B-4	Sequence 4, Appl1
26	111.8	5.5	4344	3	US-08-455-838-4	Sequence 4, Appl1
27	111.8	5.5	4344	3	US-09-019-809-4	Sequence 4, Appl1
28	111.8	5.5	4344	3	US-09-471-177-4	Sequence 4, Appl1
29	111.8	5.5	4344	3	US-09-230-806-4	Sequence 4, Appl1
30	110.8	5.5	1561	2	US-08-532-547-2	Sequence 2, Appl1
31	110.8	5.5	1561	2	US-08-379-656B-2	Sequence 2, Appl1
32	110.8	5.5	1561	3	US-08-455-838-2	Sequence 2, Appl1
33	110.8	5.5	1561	3	US-09-019-809-2	Sequence 2, Appl1
34	110.8	5.5	1561	3	US-09-471-177-2	Sequence 2, Appl1
35	110.8	5.5	1561	3	US-09-230-806-2	Sequence 2, Appl1
36	107.8	5.3	1607	3	US-08-286-870A-5	Sequence 5, Appl1
37	107.8	5.3	1946	3	US-08-286-870A-3	Sequence 3, Appl1
38	107.8	5.3	2965	2	US-08-460-570-1	Sequence 1, Appl1
39	107.8	5.3	2965	2	US-08-460-570-2	Sequence 1, Appl1
40	107.8	5.3	2965	3	US-08-286-870A-1	Sequence 1, Appl1
41	107.8	5.3	2965	3	US-08-286-870A-2	Sequence 2, Appl1
42	105.2	5.2	3507	2	US-08-315-468-3	Sequence 1, Appl1
43	104.4	5.2	4074	2	US-08-377-690-1	Sequence 1, Appl1
44	103.4	5.1	3414	2	US-07-973-320-3	Sequence 3, Appl1
45	101.8	5.0	1953	2	US-08-315-468-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-09-001-982-9
Sequence 9, Application US/09001982
Patent No. 6204246
GENERAL INFORMATION:
APPLICANT: Bosch, Hendrick J.
APPLICANT: Stiekema, Willem J.
TITLE OF INVENTION: Hybrid Toxin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6204246artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001,982
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/602,737
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3468 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3468

US-09-001-982-9

Query Match 8.5%; Score 172.4; DB 3; Length 3468;
Best Local Similarity 54.2%; Pred. No. 4,4e-33;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

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QY 161 GGGATCAGCTCGGATATATAGTAACTATGAGACATACCTTATACATCTTCTGTAAC 220
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DB 158 GCGATGACAGAAAAGAGACGATATCTATGGGACACCAATAGTCTCTTATACAGCAC 217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 221 CCGGTATAGTGAATTCCTGTAATATTTT-----CAATATATAAACCAATCCATCCGT 274
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DB 218 CTCTCTTACTGATTAATTAATTAATGATATGACCTTATAGTAAAGTACTAGAGATA 277
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QY 275 CTCTGTCATCTGTCGACGACCTTCTATATGATATTAATGATATTAATTCGTAAG 334
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DB 338 GGGTATAGTCAGATGTTTAAATGATGAGATTCAGATTTTAATGTTCTGTACTCTAT 397
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QY 395 ATCAAGATTAATTAATCTTC-----ATTATCTTGAGATTGGCTTACAGATA 439
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DB 398 ACAGAACTATTTAAGGCTCTGGATAGCTGAAATTAAGAAATCTTAATTCGCTTGCTG 457
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QY 440 AATCAATCCTTAATAAACTTGCTGAGCTAGTTAAAGCTTCCAGACGGGAGAAAGATT 499
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DB 458 AAGAACTCCGTAATCGTTTAAATGCGCAGCTCAGAAATTTGATAGAAATTTAAACCG 517
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DB 518 GGTCTTTAAGAAATGGGGCTCGTTAGCTAGACAAATGCCCCAAATTTTATTTACCTT 577
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DB 578 CTTTTGACGCGCTGCAATTTTCCATTTATTAATTAAGGATGCTACTAGATATGGCA 637
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QY 620 AAGAAATGGGACATAGTGTGCCACCGTTATCCAGGTCAGGAGAACTGATTTGTAAC 679
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DB 638 CTAAATTTGGGGCTATACAAATGCTACACCTTTTATA-----ATTATCAAT 682
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QY 680 AGCGTTAAAGCGAAATTAAGATATCTAATTTATGTAAGGTTGTTATTAACAG 739
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DB 683 CAATCTAGTAAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 742
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QY 740 GTTTAATCAGATTAAGACAGCGGGTAACTGCTGAAGTTTGGTCAAAATTTAATTAAT 799
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DB 743 GTTTCAACGAATTAAGACAGAGGACATGCTGCTACAGCTGGTTAGATTTCAATGAT 802
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QY 800 TTGCTAGAAAGTGAAGCTTGGCGGTATGATATTAATTTGCTATATTTCCAACTTATGAT 859
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DB 803 ATGCTAGAGATGACATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 862
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QY 860 TTGAAAATATTCATTAAGCAACAGTGAAGTAACTAAGGAAATTTATACAGATTCAG 919
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DB 863 TTACTATTAATCCCAATTAAGAAATGATTTTCAATGATTAAGGATTAATTAATTAATTA 922
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QY 920 TGGGATATTCAGGGGGAATTAATGTTGGGA 951
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 923 TTGGTTTGTATCATCTGATGATCTTATGGGGA 954
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```

RESULT 2

US-09-668-650-9

Sequence 9, Application US/09668650

Patent No. 6780408

GENERAL INFORMATION:

APPLICANT: Bosch, Hendrick J.

TITLE OF INVENTION: Hybrid Toxin

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

```
ADDRESSER: No. 6780408artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/668,650
FILING DATE: 22-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/001,982
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/602,737
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3468 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3468
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-668-650-9

Query Match 8.5%; Score 172.4; DB 3; Length 3468;
Best Local Similarity 54.2%; Pred. No. 4,4e-33;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 161 GGGATCAGCTCGGATATATAGTAACTATGAGACATACCTTATACATCTTCTGTAAC 220
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DB 158 GCGATGACAGAAAAGAGACGATATCTATGGGACACCAATAGTCTCTTATACAGCAC 217
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QY 221 CCGGTATAGTGAATTCCTGTAATATTTT-----CAATATATAAACCAATCCATCCGT 274
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DB 218 CTCTCTTACTGATTAATTAATTAATGATATGACCTTATAGTAAAGTACTAGAGATA 277
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QY 275 CTCTGTCATCTGTCGACGACCTTCTATATGATATTAATGATATTAATTCGTAAG 334
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DB 278 GTAGTGACATCATATGATGATTTGCTATATGATGATTAATTAATTAATTAATTAAT 337
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QY 335 AGGTAGACGAGACGCTGTTAAGTGAACGGGGTGCAGATTTTGAAGGTAATGACTGCTT 394
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DB 338 GGGTATAGTCAGATGTTTAAATGATGAGATTCAGATTTTAATGTTCTGTACTCTAT 397
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QY 395 ATCAAGATTAATTAATCTTC-----ATTATCTTGAGATTGGCTTACAGATA 439
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DB 398 ACAGAACTATTTAAGGCTCTGGATAGCTGAAATTAAGAAATCTTAATTCGCTTGCTG 457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 440 AATCAATCCTTAATAAACTTGCTGACGTTAAGTAAACAGTTCCAAAGACGGGAAAGATT 499
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 458 AAGAACTCCGTAATCGTTTAAATGCGCAGCTCAGAAATTTGATAGAAATTTAAACCG 517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 500 TCACATACTTTTACGAGGCTCATTAATCAAGACAGAAAGTGAATTTATTAATTCCTTA 559
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 518 GGTCTTTAAGAAATGGGGCTCGTTAGCTAGACAAATGCCCCAAATTTATTAATTAATTA 577
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 560 CGATGTGCAAGCTGCAAAATGCAATTATTACTATTAAAGGACGAGTTAAATATAAA 619
D 578 CTTTGGGAGCGCTGCAATTTTCCATTATTACTAAGGAGTACTGATGATGGCA 637
QY 620 AAGAAATGGGAGCTAGTGTGTCCACCGTTGTATCCAGGCTCAGGAGAACTGATGTACG 679
D 638 CTAAATGGGGCTATTAACAATGCTACACCTTTTATA-----ATTATCAT 682
QY 680 AGCGGTTAAAGCGAAATAAAGATATCTAATTAATTTGTAGGGGTATATAAAG 739
D 683 CAAACAGTAGTACTATTGAACTATTAATGATTAATGGTACATTTGGATATGAG 742
QY 740 GTTTAGATCAGATTAAGACAGCGGGGTACAGTGTGAAAGTTGTGCAAAATTAATAAT 799
D 743 GTTTCACGAACTAAGACAAAGAGGCACTAGTGTGACAGCTTGGTAAATTTTCATGAT 802
QY 800 TTGCTAGAAATGACGTTGGCGGTATTTGATATTATTTGCTATATTTTCCAACTATGAT 859
D 803 ATGCTAGAGATGACATGATGATGATTAATTAAGATGACATTCATTTTCAAGTCTGATA 862
QY 860 TTGAAAATATCCATTAGCAACAAGTATGATTAAGGAAATTTATACAGATCCAG 919
D 863 TTACTAATTAACCAATAGAAACAGATTTTCAGTTGAGTAGGCTCATTTATACAGATCCA 922
QY 920 TGGGATATTCAGGGGGAATTTATGTTGGGA 951
D 923 TTGGTTTGTACATCGTAGTGTCTTAGGGGA 954

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RESULT 3

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US-09-002-285-71
; Sequence 71, Application US/09002285
; Patent No. 6369213

```

GENERAL INFORMATION:

```

; APPLICANT: Schnef, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stockhoff, Brian
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Peets
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 71:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 3471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-002-285-71

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Query Match 8.5%; Score 172.4; DB 3; Length 3471;
Best Local Similarity 54.2%; Pred. No. 4.4e-33;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

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QY 161 GGGATCAGTCTCGATATATGATCTATTGGGACATACCTTAATCTCTGTAGAAC 220
D 158 GCGATGACAGAAAAGAGCAGTATCTATTGGGACAAACATAGTCTCTTATACAGACAC 217
QY 221 CCGGTATAGGTGAATCCCTGTAATTTT-----CAATATTAACAACATCTATCCGT 274
D 218 CTCTCTTACTGATTAATTAATTAATGATATGATGACCTTAATAGGTAAGTACTAGAGGTA 277
QY 275 CTCTGTGCAATCTGTGGCAGCAGCTTCTATATGATTAATGATCTATATTCGTAAG 334
D 278 GTAGTGAACAATCATATCAGATTTGCTATATGATGACCTTATATTTATTTGATTTAC 337
QY 335 AGGTAGCAGAGCGGTGTAATGACCGGGTTGCAATTTTGAAGGTGAATGACCTGCT 394
D 338 GGGTAAGTCAGAGGTGTTTAATGATGAGGATGACAGATTTTAATGTTCTGTACTTAT 397
QY 395 ATCAAGTTATTAATCTT-----ATTATCTGAGATTTGGCTTACAGATA 439
D 398 ACAGGAATTAATTAAGAGCTCTGATGATGATGAATTAAGAACTTAATTTGCTTGTCTG 457
QY 440 AATCAATCTTAATAAACTTGCTGACGTATGATTAACAGTTCACAGCAGGGAAGAGAT 499
D 458 AAGAACTCCGTATCTCGTTTATGATGCGCAGATTCAGATTTGATGAATTTTACCCGAG 517
QY 500 TCACTAAACTTTTACAGAGGTGATTAATCAAGACAGAAAGTGAATATTAATTTGCTGA 559
D 518 GGTCTTTAAGAAATGAGGTGCTGTTAGCTGACAAATATGCCAAATTTATTTATTAACCT 577
QY 560 CGTATGTGCAAGCTGCAAAATGCTATTTATTAATTAAGGACGCAAGTTAAATATAAA 619
D 578 CTTTGGGAGCGCTGCAATTTTCCATTATTAATTAATGATGATGATGATGATGATGATGAT 637
QY 620 AAGAAATGGGAGCTAGTGTGTCCACCGTTGATCAGGAGTCAAGGAGAACTGATGTACG 679
D 638 CTAAATGGGGCTATTAACAATGCTACACCTTTTATA-----ATTATCAT 682
QY 680 AGCGGTTAAAGCGAAATAAAGATATCTAATTAATTTGTAGGGGTATATAAAG 739
D 683 CAAACAGTAGTACTATTGAACTATTAATGATTAATGCGTACATTTGGTATATGAG 742
QY 740 GTTTAGATCAGATTAAGACAGCGGGGTACAGTGTGAAAGTTGTGCAAAATTAATAAT 799
D 743 GTTTCACGAACTAAGACAAAGAGGCACTAGTGTGACAGCTTGGTAAATTTTCATGAT 802
QY 800 TTGCTAGAAATGACGTTGGCGGTATTTGATATTATTTGCTATATTTTCCAACTATGAT 859
D 803 ATGCTAGAGATGACATGATGATGATTAATTAAGATGACATTCATTTTCAAGTCTGATA 862
QY 860 TTGAAAATATCCATTAGCAACAAGTATGATTAAGGAAATTTATACAGATCCAG 919
D 863 TTACTAATTAACCAATAGAAACAGATTTTCAGTTGAGTAGGCTCATTTATACAGATCCA 922
QY 920 TGGGATATTCAGGGGGAATTTATGTTGGGA 951
D 923 TTGGTTTGTACATCGTAGTGTCTTAGGGGA 954

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RESULT 4

```

US-09-589-477-71
; Sequence 71, Application US/09589477
; Patent No. 6570005

```

GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Micker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SRO ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-589-477-71

Query Match 8.5%; Score 172.4; DB 3; Length 3471;
Best Local Similarity 54.2%; Pred. No. 4.4e-33;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 161 GGAATCATGCTCGGATATGTAATTTGGGACATACCTTAATTTGCTGAGAC 220
DB 158 GCGATGACAGAAAGAGAGATCTAATGGACACCATAGCTCTCTTAACACAGCAC 217
QY 221 CCGGTATAGGTGGAATCTGTATATTTT-----CAATAATTAACAACCTATCCGT 274
DB 218 CTCTCTTACTGATTAATTTCAATAGTATATGACCTTAATAGGTAAGTACTAGAGAGTA 277
QY 275 CTTCGTCAATCTGTGGACGACCTTTCTATATGTGATTTAGTATCTATTAATTCGTAAG 334
DB 278 GTAGTGGACATCATATGATTTGCTATATGTGATCTATATATCATATATGATTTAC 337
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DB 398 ACAGAGACTATTTAGAGGCTCTGATAGCTGGAATTAAGAACTTAATCTGCTTCTGCTG 457
QY 440 AATCAATCTTAATAAACTTGCTGACCTAGTTAAACAGTTCCAAGCAGGGAAGAGATT 499

DB 458 AAGAACTCCGTACTGCTTTAGAAATGCGGACTCAGAAATTTGATAGAAATTTTAAACCCGAG 517
QY 500 TCACTAACTTTAGCAGGGCTATTAATCAAGACAGAAAGCTGAATATTTATTTATGCTTA 559
DB 518 GGTCTTTAAGCAATGCTGCTGCTTGAAGTACCAAAATGCCAAATATTTATTTATCTT 577
QY 560 CGTATGCACTGCAAAATGTCATTTTCTATTAAGGACGAGTAAATTAATAA 619
DB 578 CTTTGCGAGCGGTGATTTTTCATTTATTACTAAAGGATGCTACTAGATAGGCA 637
QY 620 AAGATGGGAGTATGTCACCGTGTATCCAGGCTCAGGAGAACTGATTTGAAG 679
DB 638 CTAATTTGGGGCTATATGATGCTACACCTTTATA-----ATTATCAAT 682
QY 680 AGCGTTAAAGCGAAATTAAGATATCTAATTTATTTGTTAGGCTGTATTAACAG 739
DB 683 CAAACTAGTACGCTTATTTGAACATATATGATGATTTGCTACATTTGTTAATCGAG 742
QY 740 GTTTAGATCATAGACAGGGGGTACAGTGTGCAAGTTGTCGAATTTAATAAT 799
DB 743 GTTTACAGCACTAAGACAGAGGCTAGTGTACAGCTTGTTAGAAATTCATAGAT 802
QY 800 TTCTGAGAAAATGACGTGTGCGTATTTGATATTTCTATATTTCCAACTTATGAT 859
DB 803 ATGTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 862
QY 860 TTGAAAATATTCATTTAGCAACAAGTGTAGATTAACTTGGGAAATTTATACATCCAG 919
DB 863 TTACTAATTTACCAATAGAAACAGATTTTCAGTGTAGTGGTCAATTTATACAGATCCA 922
QY 920 TGGGATATTCAGGGGGAATTTATGTTGGGA 951
DB 923 TTGCTTTTGTACATCTAGTACTTAGGGA 954

RESULT 5
US-10-099-285A-71
Sequence 71, Application US/10099285A
Patent No. 675292
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
Micker, Carol
Narva, Kenneth E.
Walz, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285A
FILING DATE: 02-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/002,285
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-099-285A-71

Query Match 8.5%; Score 172.4; DB 3; Length 3471;
Best Local Similarity 54.2%; Pred. No. 4.4e-33;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

161 GGGATCAGTCTCGATATAGTAATGAGACATACCTTATCAATTCCTGCTAGAAC 220
158 GCGATGAGCAAAAGAGACATATCTATGGGACACCATATGCTCTCTATCAGACAC 217
221 CCGGTATAGGTGGAATTCCTGTAATTTT-----CAATATAAACAACCTATTCCT 274
218 CTCTCTTACTGAGTATTAATTAATGATAGACTTATAGTAAAGTCTAGAGATA 277
275 CTCTGTCATCTGTCGACGACATCTTCTATATAGTAAATTAATTAATTCGTAAG 334
278 GTAGTGACATTCATATCAGATTTGCTATATGACTTATTAATTAATTAATTAAT 337
335 AGGTAGACGAGCGGTGTAAGTACGAGGTTGCAATTTGAGAGGTGAATGACTCTT 394
338 GGGTAAGTCAGAGTGTAAATGATGAGATGCAATTTTAATGTTGTTGTTACTCTAT 397
395 ATCAAGTTATTAATCTTC-----ATTATCTGAGATTGGCTTAACAATA 439
398 ACAGAACTATTTAGAGGCTCTGATAGCTGGAATTAAGAAATCTTAATTCGCTCTG 457
440 AATCAATCCGTAAGAACTGCTGACGATGTAACAGTTCACAGCAGGGAACAAT 499
458 AAGAACTCCGACTCGTTTGAATTCGCGACCTGACAGATTTGAATTTTAAACCGG 517
500 TCACTAACTTTTACGAGGTCATTAATCAAGACAGAAAGTGAATTAATTTGCTTA 559
518 GGTCTTAAAGAAATGAGGCTCGTTAGCTAGACAAATGCCAAATTAATTAATTA 577
560 CGTATGCAAGCTGCAATGTCATTTATTAATTAAGGACGCAATTAAATATAAA 619
578 CTCTTGGAGCGCTGCAATTTTCCATTTATTAATTAAGGATGCTAATGATAGCA 637
620 AAGAAATGGGACCTAGTGTGTCACCGTTGATCAAGGCTCAGGAGAAAGTATGTA 679
638 CTAAATGGGGCTATCAATGCTACACCTTTATTA-----ATTATCAAT 682
680 AGCGGTTAAAGCGAAATTAAGATTAATTAATTTGATGAGGTGATTAACAAG 739
683 CAAAACTAGTAGCTTATTAATTAATTAATTAATTTGATGAGGTGATTAACAAG 742
740 GTTTAGTACAGATTAAGACGAGCGGTACAAAGTCTGAAGTTTGTGCAAAATTAAT 799
743 GTTTCACGAACTAGACAAAGAGGCACTGATGCTAAGCTTGTGAAATTTCAATGAT 802
800 TTGATAGAAATGACGTTGGCGGTATGATTAATTAATTTGCAATTTCAACTAAT 859
803 ATGATAGAGATACATTAATGATTAATTAATTAATTAATTAATTTCAAGTTGATA 862
860 TTGAAAATATTCATTAAGCAACAGGTGATGATTAATTAATTAATTAATTAATCA 919
863 TTACTAATTAATCCCAATTAAGAAACAGATTTTCAAGTGAAGGTCATTTATTAAT 922
920 TGGATATTTACAGGGGGAATTAATGTTGGAA 951

Db 923 TTGTTTGTACATCGTAGTACTTAAGGGA 954

RESULT 6
US-09-001-982-11
Sequence 11, Application US/09001982
Patent No. 6204246
GENERAL INFORMATION:
APPLICANT: Bosch, Hendrick J.
APPLICANT: Stiekema, Willem J.
TITLE OF INVENTION: Hybrid Toxin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6204246artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001,982
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/602,737
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3726
US-09-001-982-11

Query Match 8.5%; Score 172.4; DB 3; Length 3726;
Best Local Similarity 54.2%; Pred. No. 4.5e-33;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

161 GGGATCAGTCTCGATATAGTAATGAGACATACCTTATCAATTCCTGCTAGAAC 220
158 GCGATGAGCAAAAGAGACATATCTATGGGACACCATATGCTCTCTATCAGACAC 217
221 CCGGTATAGGTGGAATTCCTGTAATTTT-----CAATATAAACAACCTATTCCT 274
218 CTCTCTTACTGAGTATTAATTAATGATAGACTTATAGTAAAGTCTAGAGATA 277
275 CTCTGTCATCTGTCGACGACATCTTCTATATAGTAAATTAATTAATTCGTAAG 334
278 GTAGTGACATTCATATCAGATTTGCTATATGACTTATTAATTAATTAATTAAT 337
335 AGGTAGACGAGCGGTGTAAGTACGAGGTTGCAATTTGAGAGGTGAATGACTCTT 394
338 GGGTAAGTCAGAGTGTAAATGATGAGATGCAATTTTAATGTTGTTGTTACTCTAT 397
395 ATCAAGTTATTAATCTTC-----ATTATCTGAGATTGGCTTAACAATA 439

Db 398 ACAGAACTATTAGAGGCTCTGGATGAGTGAATAAGATTCCTAATTCCTCTGCTG 457
 QY 440 AATCAATCTTAAAAAAGCTGCGAGCTACTTAACAGTTCCAGACCGGAAAGATT 499
 Db 458 AAAAACTCCGCTACTCGTTTGAATCCGCCACCTCAGATTTGATGATTTTAAACCGAG 517
 QY 500 TCACTAACTTTAGCAGGCTCATTTATCAAGACGAAAGCTGAATTTATTTATGCGCTA 559
 Db 518 GGTCTTTAAGAAATGGGCTCGTACTAGTACAAATGCCCCAATTTATTTACCTT 577
 QY 560 CGTATGCAAGCTGCAATGTGCATTTATTAAGGAGCGAGTTAAATATATATAT 619
 Db 578 CTTTGGAGCGCTGCATTTTCCATTTATTAAGGATGCTAGATGATGCA 637
 QY 620 AAGAAATGGGAGCTAGTGTGCTCCACCTGTATCCAGGCTCAGGAGACCTGATTTGACG 679
 Db 638 CTAAATGGGGGCTATACAAATGCTACACCTTTATTA-----ATTATCAAT 682
 QY 680 AGCGTTAAAAAGCAAAATTAAGATGATCTAATTTGTGTAGGGTGGTATACAGG 739
 Db 683 CAAACTAGTAGGCTTATGAACTATTAATCTGATTTGCGTACATGGTATATACGAG 742
 QY 740 GTTTAGATCAGATPAGACAGCGGGTACAAAGTGTGAAGTTTGGTCAAAATTTAATTAAT 799
 Db 743 GTTTCACGAACTAAGCAACAGGCACTAGTGTACAGCTGTGATGAAATTTCAATAGAT 802
 QY 800 TTGGTAGAAGAAATGCGTGGCGTATGGATTAATTTGCTATATTTCCACTATAGAT 859
 Db 803 ATGTGAGAGATGACATGATGTATTAATGATAGATCATCAATTTCAAGCTTGATA 862
 QY 860 TTGAAAAATATCATTAAGCAACAGTGTAGATTAAGGAAATTTATACAGATCCAG 919
 Db 863 TTACTAATTAACCAATAGAAAACAGATTTTCAGTTGATAGGTCATTTATACAGATCCA 922
 QY 920 TGGGATATTCAAGGGGAAATTAATGTTGGGAA 951
 Db 923 TTGGTTTGTACATCTGATAGTCTTGGGGA 954

RESULT 7

US-09-668-650-11
 ; Sequence 11, Application US/09668650
 ; Patent No. 6780408
 ; GENERAL INFORMATION:
 ; APPLICANT: Bosch, Hendrick J.
 ; TITLE OF INVENTION: Hybrid J.
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: No. 6780408artis Corporation
 ; STREET: 3054 Cornwallis Road
 ; CITY: Research Triangle Park
 ; STATE: NC
 ; COUNTRY: USA
 ; ZIP: 27709
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/668,650
 ; FILING DATE: 22-Sep-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/001,982
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US 08/602,737
 ; FILING DATE: 21-FEB-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meigs, J. Timothy
 ; REGISTRATION NUMBER: 38,241
 ; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-541-8587
 ; TELEFAX: 919-541-8689
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3726 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..3726
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 US-09-668-650-11
 Query Match 8.5%; Score 172.4; DB 3; Length 3726;
 Best Local Similarity 54.2%; Pred. No. 4,5e-33;
 Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;
 Db 161 GGAATCAATCTCGATATAGTAACTATTGGGACATCTTATACAAATCTTGCTAGAAC 220
 QY 158 GCGATGCAACAAAGAGCAGATCTATTGGGACAAACATAGCTCTCTTATCAGACGAC 217
 Db 221 CCGGTATAGTGAATTCCTGATATATTT-----CAATATTAACAACATCATTCGCT 274
 QY 218 CTTCCTTACTGATTAATTTCAATAGTATAGACCTTATAGCTTAAAGTACAGAGTA 277
 Db 275 CTTCGTGCAATCTGTGAGCAGCTTTCTAATGTGATTTAGTATCTAATATTCGTAAG 334
 QY 278 GTATGAGCAATTCATATACAGATTTGCTAATGTGACTTAATTAATCTAATTAATGATTC 337
 Db 335 AGGTAGACAGACCGCTTTAAGTACGAGGCTGCAATTTTGAAGGTGAATAGATCGCT 394
 QY 338 GGGTATGACAGTGTTTTAAATGATGGATGACAGATTTTAATGATGCTGATCTTAT 397
 Db 395 ATCAAGATTAATATCTTC-----ATTATCTGAGATTTGGCTTACAGATA 439
 QY 398 ACAGAACTATTAGAGGCTCTGATAGCTGAAATTAAGATCTTAATTCGTTCTGCTG 457
 Db 440 AATCAATCTTAAAAAAGCTGCTGACGATTAACAGTTCCAGACCGGAAAGATT 499
 QY 458 AAAAACTCCGCTACTCGTTTGAATCCGCCACCTCAGATTTGATGATTTTAAACCGAG 517
 Db 500 TCACTAACTTTAGCAGGCTCATTTATCAAGACGAAAGCTGAATTTATTTATGCGCTA 559
 QY 518 GGTCTTTAAGAAATGGGCTCGTACTAGTACAAATGCCCCAATTTATTTATTAACCTT 577
 Db 560 CGTATGCAAGCTGCAATGTGCATTTATTAAGGAGCGAGTTAAATATATATAT 619
 QY 578 CTTTGGAGCGCTGCATTTTCCATTTATTAAGGATGCTAGATGATGCA 637
 Db 620 AAGAAATGGGAGCTAGTGTGCTCCACCTGTATCCAGGCTCAGGAGACCTGATTTGACG 679
 QY 638 CTAAATGGGGGCTATACAAATGCTACACCTTTATTA-----ATTATCAAT 682
 Db 680 AGCGTTAAAAAGCAAAATTAAGATGATCTAATTTGTGTAGGGTGGTATACAGG 739
 QY 683 CAAACTAGTAGGCTTATGAACTATTAATGATGATGATGATGATGCA 742
 Db 740 GTTTAGATCAGATPAGACAGCGGGTACAAAGTGTGAAGTTTGGTCAAAATTTAATTAAT 799
 QY 743 GTTTCACGAACTAAGCAACAGGCACTAGTGTGCTACAGCTTTGATGATGATGCA 802
 Db 800 TTGGTAGAAGAAATGCGTGGCGTATGGATTAATTTGCTAATTTCCACTATAGAT 859
 QY 803 ATGTGAGAGATGACATGATGTATTAATGATAGATGATGATGATGCA 862
 Db 860 TTGAAAAATATCATTAAGCAACAGTGTGATGATTAAGGAAATTTATACAGATCCAG 919
 QY 863 TTACTAATTAACCAATAGAAAACAGATTTTCAGTTGATAGGTCATTTATACAGATCCA 922
 Db 920 TGGGATATTCAAGGGGAAATTAATGTTGGGAA 951

Oy 915 TCCAGTGGGATATT CAGGGGAAATTATGGTTGGGAACGGTTTTTTTAGCTTTAAT 969
| | | | |
Db 867 TCCAATTGGGAGAACCAATGCATT CAGGATTTGCAGACTACGAATGTGTTTAAT 921
| | | | |

RESULT 10

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US-08-100-709-3
: Sequence 3, Application US/08100709
: Patent No. 5322687
:
: GENERAL INFORMATION:
: APPLICANT: Donovan, William P.
: APPLICANT: Tan, Yuding
: APPLICANT: Jany, Christine S.
: APPLICANT: Gonzalez Jr., Jose M.
: TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
: TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
: ADDRESSEE: Nadel
: STREET: 1601 Market Street, 36th Floor
: CITY: Philadelphia
: STATE: Pennsylvania
: COUNTRY: U.S.A.
: ZIP: 19103
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/100,709
: FILING DATE: 19930729
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Egolf, Christopher
: REGISTRATION NUMBER: 27633
: REFERENCE/DOCKET NUMBER: 7205-49
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-757-1590
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3934 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: circular
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 67..3756
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 2253..2272
:
US-08-100-709-3

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Db	672	TGGTATGTAATGGGGATGGCATCTTCCGATGTTAACCA-----TA	71.3
Qy	675	TAAcGAGCGGTTAAAAGCAAAATTAAGAAGTATCTATATTGTGAGGGTGTTAA	73.4
Db	714	TTTACCAAGAACAAATTCAGTATATACAGAGAAATATTCTTACATTGCGTACAAATGGTTTAA	77.3
Qy	735	CAAGGTTTAGATTCAGATNAGAACAAGCGGATCAAGTCTGAAAGTTGGTGCAAATTAA	79.9
Db	774	TACAGGCTTAATTAACCTTAGA-----GGGCAAAATGCTGAAGTTGGTGCGTATA	82.7
Qy	795	TAAATTTGCTAAGAAATGACGTTGGCGGTATTGATTTATATGCTATATTTCCACTTA	85.5
Db	828	TCATTTCCGTAGAGACTTACGTTAGGGGTATTAGATTTTATGATCCCTATATCCCAACTA	88.7
Qy	855	TGATTTGAAAAATATCCATTAGCAACAAGTGTAGTTAACTAGGAAATTTTACAGA	91.4
Db	888	TGATATCTCGCACTTATCCAAATCAATACAGAGTCTCAGTTAACAGAGAAATTTTATACAGA	94.7
Qy	915	TCAGAGGGAATNTACAGGGGAAATTAATGTTGGAAACGTTTTTGGCTTAAT	96.9
Db	948	TCCAAATTTGGAGAACAAATGACCTTCAGAGATTTCAGATNAGCAATTTGGTTTTAAT	100.2

RESULT 11

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US-08-176-865-3
Sequence 3, Application US/08176865
Patent No. 5616319
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Yan, Yaping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-176,865
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3934 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 67..3756
FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: 2253..2272
US-08-176-865-3

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Query Match	5.9%;	Score 118.2;	DB 2;	Length 3934;
Best Local Similarity	54.8%;	Pred. No. 1.6e-19;		
Matches 293; Conservative	0;	Mismatches 218;	Indels 24;	Gaps 2;

OY	435	AGATTAATCAAAATCCTTAATAAAAACTTGTCAGCTAGTTAAACGTTTCAAGACGGGAA	494
Db	492	AGATTAACCGAANTGATGCAAGATCAAGAAGCAATTATCTTGAGCCGTATGTGCTTTGA	551
OY	495	AGATTTCACCTAACTTTTAGCAGGGTCATTATCAAGACAGAAGCTGAATATATTAAT	554
Db	552	ACTTGACATTTACTGCTATATCCGCTTTTCAGAAATACGAATGGAAGAGTTCCATTAT	611
OY	555	GCTTACGTATGTGCAAGCTGCAAATGTGCATTATTAATTAATTAAGGACGCAGTTAAAT	614
Db	612	AATGGTATATGCTCAAGCTGCMAATTTACACTTATTAATTATGAGAGCGATCCCTTT	671
OY	615	TAAAAAAGATGGGGACTATGTGTCCACCGTTTATCAGGGGTACGGGAACGATGTTG	674
Db	672	TGTTAGTAAATGGGGGATGGCATCTTCGATGTAAACAA-----TA	713
OY	675	TAAAGAGGGTTAAAGAGGAAATTAAGAAGTATCTAATTAATTTGTAGGGTGGTATTA	734
Db	714	TTACCAGAACAATCAAGATATACAGAGGAATATTTCAACCTTCGTACATGGTATTA	773
OY	735	CAAGGGTTTGAATCAGATTAAGCAGAGCGGGTCAAGTCTGAAGTTTGGTGCMAATTTAA	794
Db	774	TACAGGGTAAATAACTTTAAGA-----GGACAATAGCTGAAGATTTGGTGGGTATTA	827
OY	795	TAAATTTGATAGAGAAATGACGTGGCGGTATTTGATATTTATTTGCTATATTTCCAATTA	854
Db	828	TCAATTCGTTAGAGACTTAACGTTTAGGGGTATTAATTTAGTAGCCCATTTCCCAAGCTA	887
OY	855	TGATTTTGAATAAATATCCATTAGCAACAAGTGTAGAGTTAACTAGGAGAAATTTATACGA	914
Db	888	TGATTAATCGCACTTATCCAAATCAATACAGAGTGCAGTTTAAACAAGAGAAATTTATACGA	947
OY	915	TCCAGTGGGATTAATCAGGGGAAATTAATGTGTGGGAACGTTTTTTTACTTTAAT	969
Db	948	TTCAATTTGGGAGAAACAAATGCACTTCACGATTTGCAAGTATTCGAATTTGGTTTTAAT	1002

RESULT 12
 US-08-474-038-3
 Sequence 3, Application US/08474038
 Patent No. 5679343
 GENERAL INFORMATION:
 APPLICANT: Donovan, William P.
 APPLICANT: Tan, Yoping
 APPLICANT: Jany, Christine S.
 APPLICANT: Gonzalez Jr., Jose M.
 TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYE4 AND CRYE5
 TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOTERAN INSECTS
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
 ADDRESSEE: Nadel
 STREET: 1601 Market Street, 36th Floor
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: U.S.A.
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,038
 FILING DATE: 07-JUN-1995

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? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/176,865
? FILING DATE: 30-DEC-1993
? APPLICATION NUMBER: US 08/100,709
? FILING DATE: 29-JUL-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: BOLF, Christopher
? REGISTRATION NUMBER: 27633
? REFERENCE/DOCKET NUMBER: 7205-49
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 215-757-1530
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 3934 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 67..3756
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: 2253..2272
?
US-08-474-038-3

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Query Match	5.9%	Score 118.2;	DB 2;	Length 3934;
Best Local Similarity	54.8%;	Pred. No. 1.6e-19;		
Matches 293;	Conservative 0;	Mismatches 218;	Indels 24;	Gaps 2;

OY	435	AGATTAATTCAAATCTCTAAAAAACTTGTGACGTAAGTAAACAGTTCACAGACGGGAGAA	496
Db	492	AGATTAACCGAAATATATCAGATATCAAGACATTAATCTTGAAGCGCTATGCTTTTAA	551
OY	495	AGATTTCACTAAACTTTTAAACAGGGTCATTATCAAGACAGAAAAGCTGAAATATTATTAT	554
Db	552	ACTTGACATTACTCTACTCTATTACCGCTTTTCAGAAATCGAAATGAAAGAGTTCATTATT	611
OY	555	GCTACGTAATGTGCAAGCTGCAAAATGTCATTTTATCTATTAAAGGAACGCAAGTAAATA	614
Db	612	AATGCTATTATGCTCAAGCTGCAAAATTTACCTTAATTATATGAGAACGATCCCTTTT	671
OY	615	TAAAAAAGAAATGGGGACTAGTGTGTCCACCGTTGATCCAGGTCAGAGGAACGTGATG	674
Db	672	TGTAGTGAATATGGGGATGCGATCTTCCAGTGTAAACCA-----TAA	713
OY	675	TAAAGACGGTTTAAACGAAATTTAAAGATTAATCTAAATTAATTGTGTAGGCGTATA	734
Db	714	TTACCAAGAAACAAATTCAGATTAACAGAGAAATTTCTAACCAATTCGCTCAATGATATA	773
OY	735	CAAGGTTTATGATCAGATTAAGACAGGGCGGTACAGGTCTGAAGTTTGTGCAAAATTAA	794
Db	774	TACAGGGCTAAATTAATCTTAAGA-----GGACAAATGCTGAAGATTGTTGGCGTATA	827
OY	795	TAAATTTCTGATAGAAATGACGTTGGGGGTATTGGAATTAATTGCTAATTTTCCAATTAA	854
Db	828	TCAATTTCCGATAGAACCTTAACGTTAAGGGGATTAAGATTAGTAGCCCTAATTTCCAACTTA	887
OY	855	TGATTTTGAAGAAATATCTATTAGCAACAAGTGTAGATTAACTAAGGAAATTTTATACAGA	914
Db	888	TGATTAATCGCACTTATTCATTCAAATTCAGATGTGCTCACTTAACAAGAAATTTATACAGA	947
OY	915	TCCAGTGGGAATTTCAAGGGGAAATTAATGTTGGGAACGTTTTTAACTTTAAT	969
Db	948	TCCATTTGGGAGAACCAATGCACTTCAGGATTTTGCAAGTACGAATGTTTAAAT	1002

RESULT 13
US-08-779-046-3
; Sequence 3, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:

APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuding
APPLICANT: Jany, Christine S. M.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Panlitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSER: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,046
FILING DATE: 06-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egoif, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3934 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 67..3756
FEATURE:
NAME/KEY: misc feature
LOCATION: 2253..2272
US-08-779-046-3

Query Match 5.9%; Score 118.2; DB 2; Length 3934;
Best Local Similarity 54.8%; Pred. No. 1.6e-19;
Matches 293; Conservative 0; Mismatches 218; Indels 24; Gaps 2;

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QY 495 AGATTCACCTAACTTTAGCAGGCTATTAATCAAGCAGAAAGCTGAATATTATTAT 554
DB 552 ACTTGACATTACTACGCTATACCGCTTTTCAGAAATGAAAGAAATTCATTAAT 611
QY 555 GCCTACGTATGTCAGAGCTCAAAATGTCATTTATTACTTAAGGAGCGAGTTAAATA 614
DB 612 AATGCTATATGCTCAAGCTGCAAAATTTACACCTATTATTATTGAGAGACCAATCCCTTT 671
QY 615 TAAAAAAGATGGGAGCTAGTGTCACCGCTGTATCCAGGCTCAGGAGAACTGATTG 674
DB 672 TGGTAGAATGGGGAGTGCATCTTCGATGTTAACCA-----TA 713
QY 675 TAAAGAGCGGTTAAAAACGAAATAAAGATATACATTAATTGTTAGGCTGATTA 734
DB 714 TTACCAAGAAACAATCATGATATACAGAGATATTTTACCATTTGCGTACAAATGGTATTA 773
QY 735 CAAGGTTTATGATCAGATAAGACAGCGGGTACAAAGTGTGAAGTTTGTGCAATTTTA 794

DB 774 TACAGGCTAAATTAAGT-----GGACAAATGCTGAAGTTGTCGGTATTA 827
QY 795 TAAATTCGTAGAGAAATGACGTGGCGTATGTAATTAATTTTCAACTTA 854
DB 828 TCAATTCGTAGAGAAATGACGTGGCGTATGTAATTAATTTTCAACTTA 887
QY 855 TCAATTCGTAGAGAAATGACGTGGCGTATGTAATTAATTTTCAACTTA 914
DB 888 TCAATTCGTAGAGAAATGACGTGGCGTATGTAATTAATTTTCAACTTA 947
QY 915 TCAATTCGTAGAGAAATGACGTGGCGTATGTAATTAATTTTCAACTTA 969
DB 948 TCAATTCGTAGAGAAATGACGTGGCGTATGTAATTAATTTTCAACTTA 1002

RESULT 14
US-08-881-340-3
Sequence 3, Application US/08881340
Patent No. 5942658
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuding
APPLICANT: Jany, Christine S. M.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Panlitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSER: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,340
FILING DATE: 24-JUN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egoif, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3934 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 67..3756
FEATURE:
NAME/KEY: misc feature
LOCATION: 2253..2272
US-08-881-340-3

Query Match 5.9%; Score 118.2; DB 2; Length 3934;
Best Local Similarity 54.8%; Pred. No. 1.6e-19;
Matches 293; Conservative 0; Mismatches 218; Indels 24; Gaps 2;

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1      FILING DATE: 13-SEPT-1991
2      CLASSIFICATION: 424
3      ATTORNEY/AGENT INFORMATION:
4      NAME: Salivanchik, David R.
5      REGISTRATION NUMBER: 31,794
6      REFERENCE/DOCKET NUMBER: M/S 102D.CI
7      TELECOMMUNICATION INFORMATION:
8      TELEPHONE: (904) 375-8100
9      TELEFAX: (904) 372-5800
10     INFORMATION FOR SEQ ID NO: 7:
11     SEQUENCE CHARACTERISTICS:
12     LENGTH: 3684 base pairs
13     TYPE: nucleic acid
14     STRANDEDNESS: single
15     TOPOLOGY: linear
16     MOLECULE TYPE: DNA (genomic)
17     US-08-446-170-7

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Query Match	5.8%;	Score 116.8;	DB 2;	Length 3684;
Best Local Similarity	55.0%;	Pred. No. 3.4e-19;		
Matches 310; Conservative	0;	Mismatches 227;	Indels 27;	Gaps 3;

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Oy	826	TTGATATTTATTTGCTATATTTTCCAATTAATGATTTTGAATAATATTCATTAGCAACAAGT	885
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Search completed: December 19, 2005, 13:03:21
Job time : 256.648 secs

Handwritten text, possibly a signature or name, oriented vertically.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:29:27 ; Search time 1166.77 Seconds

(without alignments)
15202.512 Million cell updates/sec

Title: US-10-782-141-1

Perfect score: 1 tttcaccacaataatcatgtt.....atagttatcatcaataa 2145

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_NA_Main:*

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- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2019	94.1	2019	US-10-782-141-2	Sequence 2, Appl1
3	2010	93.7	2010	US-10-782-141-4	Sequence 4, Appl1
4	855	39.9	5980	US-10-781-979-1	Sequence 1, Appl1
5	747.2	34.8	2082	US-10-781-979-2	Sequence 2, Appl1
6	739.4	34.5	2073	US-10-781-979-4	Sequence 4, Appl1
7	172.4	8.0	3471	US-10-099-285-71	Sequence 71, Appl1
8	162.8	7.6	2407	US-10-428-961-29	Sequence 29, Appl1
9	133.6	6.2	4391	US-10-929-754-4	Sequence 4, Appl1
10	119.8	5.6	1959	US-10-428-961-5	Sequence 5, Appl1
11	117.6	5.5	1808	US-10-782-020-4	Sequence 4, Appl1
12	117.6	5.5	1890	US-10-782-020-2	Sequence 2, Appl1
13	116.8	5.5	2190	US-10-782-020-1	Sequence 1, Appl1
14	116.8	5.4	3684	US-10-428-961-62	Sequence 62, Appl1
15	113.4	5.3	2019	US-10-665-460A-7	Sequence 7, Appl1
16	112.4	5.2	3687	US-10-614-524-1	Sequence 1, Appl1
17	112.4	5.2	4173	US-10-428-961-17	Sequence 3, Appl1
18	111.8	5.2	2019	US-10-665-460A-1	Sequence 1, Appl1
19	111.8	5.2	2019	US-10-665-460A-3	Sequence 3, Appl1
20	111.8	5.2	3471	US-10-099-285-73	Sequence 73, Appl1
21	111.8	5.2	3471	US-10-428-961-27	Sequence 27, Appl1
22	111.8	5.2	4344	US-10-687-879A-4	Sequence 4, Appl1
23	110.8	5.2	1561	US-10-687-879A-2	Sequence 2, Appl1

24	110.2	5.1	2019	7	US-10-665-460A-5	Sequence 5, Appl1
25	105.4	4.9	2019	7	US-10-665-460A-11	Sequence 11, Appl1
26	105	4.9	1860	5	US-10-032-717-19	Sequence 19, Appl1
27	105	4.9	1860	6	US-10-414-637-19	Sequence 19, Appl1
28	105	4.9	1860	7	US-10-606-320-15	Sequence 15, Appl1
29	105	4.9	1860	8	US-10-746-914-15	Sequence 15, Appl1
30	105	4.9	2003	5	US-10-032-717-5	Sequence 5, Appl1
31	105	4.9	2003	6	US-10-414-637-5	Sequence 5, Appl1
32	105	4.9	2010	6	US-10-032-717-15	Sequence 15, Appl1
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36	105	4.9	3621	5	US-10-032-717-1	Sequence 1, Appl1
37	105	4.9	3621	6	US-10-414-637-1	Sequence 1, Appl1
38	105	4.9	3621	7	US-10-606-320-1	Sequence 1, Appl1
39	105	4.9	3621	8	US-10-746-914-1	Sequence 1, Appl1
40	105	4.9	3621	10	US-11-021-115-5	Sequence 5, Appl1
41	105	4.9	4874	5	US-10-032-717-27	Sequence 27, Appl1
42	105	4.9	4874	6	US-10-414-637-27	Sequence 27, Appl1
43	105	4.9	4874	7	US-10-606-320-17	Sequence 17, Appl1
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ALIGNMENTS

RESULT 1
US-10-782-141-1
; Sequence 1, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargis, Tracy
; APPLICANT: Kozel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; FILE REFERENCE: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: *Bacillus thuringiensis*
US-10-782-141-1

Query Match 100.0%; Score 2145; DB 8; Length 2145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTTCCACCAATATATATGTTTTTTTGTAGAAACCTGTTCAGGAATATACATTTGGGTACTA 60
1 TTTCCACCAATATATATGTTTTTTTGTAGAAACCTGTTCAGGAATATACATTTGGGTACTA 60
61 CGAATATATAGAAAGACACCTGGCATATATTTATAGGTCTTTAAATATAGACTATA 120
61 CGAATATATAGAAAGACACCTGGCATATATTTATAGGTCTTTAAATATAGACTATA 120
121 TAAAGAGTGAATAATATGATTTCTTATCAAAATAGAAATGAAATATTCGATGCT 180
121 TAAAGAGTGAATAATATGATTTCTTATCAAAATAGAAATGAAATATTCGATGCT 180
181 TCCCGCAATATACCAATATATGTCAGAACAGATATCTTTTGCAGAGATCCAAATATATTT 240
181 TCCCGCAATATACCAATATATGTCAGAACAGATATCTTTTGCAGAGATCCAAATATATTT 240
241 CCTATTAACTGGACGCTTGTCAGGAGGCCATGGCAAGATATCGTGGAAATCATGCTCG 300

Db 241 CCTATTAACTGGACGCTTGTGACGGAAAGCCATGGCAATGCGTGGAAATCAAGCTCG 300
Qy 301 GATATAGTACTATTTGGGACATACCTTATACAAATCTTCTGTAAGACCGGATAGGTGGA 360
Db 301 GATATAGTACTATTTGGGACATACCTTATACAAATCTTCTGTAAGACCGGATAGGTGGA 360
Qy 361 ATTCCGCTATATTTTCAATATATAAACAATCCATTCGGTCTTCTGGTCAATCTGGGCA 420
Db 361 ATTCCGCTATATTTTCAATATATAAACAATCCATTCGGTCTTCTGGTCAATCTGGGCA 420
Qy 421 GCACTTCTATATGTGATTTAGTATCTAATTCGTAAAGAGGTAGACGAGACGCTGTA 480
Db 421 GCACTTCTATATGTGATTTAGTATCTAATTCGTAAAGAGGTAGACGAGACGCTGTA 480
Qy 481 AGTACGCGGGGTGCAAGTTTGAAGGTGAATGACGTCTTATCAAGATTTATTTCTTCAT 540
Db 481 AGTACGCGGGGTGCAAGTTTGAAGGTGAATGACGTCTTATCAAGATTTATTTCTTCAT 540
Qy 541 TATCTTGAGGATTTGCTTACAGATTAATCAATCCCTAAAAAACTTGTGACGTAGTTAA 600
Db 541 TATCTTGAGGATTTGCTTACAGATTAATCAATCCCTAAAAAACTTGTGACGTAGTTAA 600
Qy 601 CAGTCCAGACGCGGAGAAAGATTCTAATACTTTTACAGAGGTCAATATCAAGACAG 660
Db 601 CAGTCCAGACGCGGAGAAAGATTCTAATACTTTTACAGAGGTCAATATCAAGACAG 660
Qy 661 AAAGCTGAATATATATATATGCTTACGATGTCAGAGTCAAGTCAATGCTTTATTA 720
Db 661 AAAGCTGAATATATATATATGCTTACGATGTCAGAGTCAAGTCAATGCTTTATTA 720
Qy 721 TTAAGGAGCAGTAAATATATAAAGAAATGAGGAGTACAGTGTGCTCAAGCTTATCA 780
Db 721 TTAAGGAGCAGTAAATATATAAAGAAATGAGGAGTACAGTGTGCTCAAGCTTATCA 780
Qy 781 GGGTCAGAGAACTGATTTGTAACGAGCGGTTAAACCGAAAAATAAAGATATCTAAT 840
Db 781 GGGTCAGAGAACTGATTTGTAACGAGCGGTTAAACCGAAAAATAAAGATATCTAAT 840
Qy 841 TATGCTAGGCTGCTTAAACAGGCTTATGATCAGATTAAGACAGGCGGTACAGTGT 900
Db 841 TATGCTAGGCTGCTTAAACAGGCTTATGATCAGATTAAGACAGGCGGTACAGTGT 900
Qy 901 GAAGTTGCTGCAAAATTTAATTTCTGTAAGAAATGAAGTGGCGGTATTTGATAT 960
Db 901 GAAGTTGCTGCAAAATTTAATTTCTGTAAGAAATGAAGTGGCGGTATTTGATAT 960
Qy 961 ATTGCTATATTTCCAACTTATGATTTTGAATAATATCATTAGCAACAGTGTAGATTA 1020
Db 961 ATTGCTATATTTCCAACTTATGATTTTGAATAATATCATTAGCAACAGTGTAGATTA 1020
Qy 1021 ACTAGGGAATTTATACAGATCCAGTGGGATTTCAAGGGGAAATTTGTTGGGAACGG 1080
Db 1021 ACTAGGGAATTTATACAGATCCAGTGGGATTTCAAGGGGAAATTTGTTGGGAACGG 1080
Qy 1081 TTTTGTAGCTTAAATTCGTAGAAAGCAATGGAACAGCGGGAACCTGGTTAGTTACTGG 1140
Db 1081 TTTTGTAGCTTAAATTCGTAGAAAGCAATGGAACAGCGGGAACCTGGTTAGTTACTGG 1140
Qy 1141 CTTCAAGCTATAGATATATAGTCAATTTATTTCAAGCTTGTGTTATCTTATGAGC 1200
Db 1141 CTTCAAGCTATAGATATATAGTCAATTTATTTCAAGCTTGTGTTATCTTATGAGC 1200
Qy 1201 TGGGGGGGAACTGCTATATGAAAGCTTCAAAAGGGTAAACGGTGTCTTTTCAACGTATG 1260
Db 1201 TGGGGGGGAACTGCTATATGAAAGCTTCAAAAGGGTAAACGGTGTCTTTTCAACGTATG 1260
Qy 1261 TCTGGAATCAGATATATATCCAGTATATTTTGGCAATATCCGATATATTTAA 1320
Db 1261 TCTGGAATCAGATATATATCCAGTATATTTTGGCAATATCCGATATATTTAA 1320
Qy 1321 ATTATTTCAATAGCTAGATATGCAATCAACCGTTGTGGGTATTCATCCACGGCAT 1380
Db 1321 ATTATTTCAATAGCTAGATATGCAATCAACCGTTGTGGGTATTCATCCACGGCAT 1380

Db 1321 ATTATTTCAATAGCTAGATATGCAATCAACCGTTGTGGGTATTCATCCACGGCAT 1380
Qy 1381 CTTGTTTACCGTGCAGAAATTTTTCGACAAACCTTAATACTTCTCTGATATAGGTTAAC 1440
Db 1381 CTTGTTTACCGTGCAGAAATTTTTCGACAAACCTTAATACTTCTCTGATATAGGTTAAC 1440
Qy 1441 AGTTGCGGATCTCAGACAAATTTGATCTGATACAGAGATTTAATTAAGATCTACCA 1500
Db 1441 AGTTGCGGATCTCAGACAAATTTGATCTGATACAGAGATTTAATTAAGATCTACCA 1500
Qy 1501 CCTAGTCTTACAAATTTCTCATGATATTAATCAATGCGGACGTGTTCAAAATGAAAC 1560
Db 1501 CCTAGTCTTACAAATTTCTCATGATATTAATCAATGCGGACGTGTTCAAAATGAAAC 1560
Qy 1561 TCCAGAGTTAAAGTATTTGGTTGGACATACAAATTAAGAAAGATTAATGAAATTTAT 1620
Db 1561 TCCAGAGTTAAAGTATTTGGTTGGACATACAAATTAAGAAAGATTAATGAAATTTAT 1620
Qy 1621 CCAGATTAATTAATTAATTTCTGCAATTAAGCTTTTCCCTACAGACAGTACAGGA 1680
Db 1621 CCAGATTAATTAATTAATTTCTGCAATTAAGCTTTTCCCTACAGACAGTACAGGA 1680
Qy 1681 TATGACAGAGTTACGTCACAGCTGCGCTGTTATTAACAGAGAGATGTATTAAGTTA 1740
Db 1681 TATGACAGAGTTACGTCACAGCTGCGCTGTTATTAACAGAGAGATGTATTAAGTTA 1740
Qy 1741 CCTTATCAAGCAAGTTTAAATATAGTTTAACTTCTGCAACCAAGATTAATTAACGT 1800
Db 1741 CCTTATCAAGCAAGTTTAAATATAGTTTAACTTCTGCAACCAAGATTAATTAACGT 1800
Qy 1801 GTTAACTTCGCTACGCGAGTGAAGAACTGCTGCTTCCGATGCGGATGAGTGTGCGCA 1860
Db 1801 GTTAACTTCGCTACGCGAGTGAAGAACTGCTGCTTCCGATGCGGATGAGTGTGCGCA 1860
Qy 1861 AGTCTGTTTCAAAATGCTAATTTTCTGCTCAGCTACAGGTGCGCTATATGTTCAAT 1920
Db 1861 AGTCTGTTTCAAAATGCTAATTTTCTGCTCAGCTACAGGTGCGCTATATGTTCAAT 1920
Qy 1921 TATGTCGACACTTGTATCTATCAATTTAATCAATCAAGGTGGAATATTTATTAACAAAT 1980
Db 1921 TATGTCGACACTTGTATCTATCAATTTAATCAATCAAGGTGGAATATTTATTAACAAAT 1980
Qy 1981 CTATCTGTTTACCACTTATGTTTGAACAAAGTCAATTTATCCCAATGACATCCAAAT 2040
Db 1981 CTATCTGTTTACCACTTATGTTTGAACAAAGTCAATTTATCCCAATGACATCCAAAT 2040
Qy 2041 GAAAAATGTAAGAAATGTCATTTGGAAGGACATATGTAGTGTGAAGAGTACATCC 2100
Db 2041 GAAAAATGTAAGAAATGTCATTTGGAAGGACATATGTAGTGTGAAGAGTACATCC 2100
Qy 2101 TTGGAACAAAAAAGAGTTGTAAATAGTTTATTTATCAATTTAA 2145
Db 2101 TTGGAACAAAAAAGAGTTGTAAATAGTTTATTTATCAATTTAA 2145

RESULT 2
US-10-782-141-2
; Sequence 2, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargis, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; TITLE OF INVENTION: Axmi-014, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; PRIOR APPLICATION NUMBER: 2004-02-20
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23

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SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-10-782-141-2

Query Match      94.1%; Score 2019; DB 8; Length 2019;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      127 GTGAAAAATATGAAATCTTATCAAAATPACAAATGAAATGAAATTCGATGCTGCCG 186
Db      1 GTGAAAAATATGAAATCTTATCAAAATPACAAATGAAATGAAATTCGATGCTGCCG 60

QY      187 AATPACAAATATGCAATGCAAGTATCCCTTTGCAAGAGTCCAAATATATTCCTAT 246
Db      61 AATPACAAATATGCAATGCAAGTATCCCTTTGCAAGAGTCCAAATATATTCCTAT 120

QY      247 AACCTGACGCTTGTCAAGGAGGCGATGGCAAGATCGTGGGAATGAGTCTGGATATA 306
Db      121 AACCTGACGCTTGTCAAGGAGGCGATGGCAAGATCGTGGGAATGAGTCTGGATATA 180

QY      307 GTAACTATGAGGACATACCTTATACAAATTCCTGCTAGAACCCGGTATAGGTGAAATCT 366
Db      181 GTAACTATGAGGACATACCTTATACAAATTCCTGCTAGAACCCGGTATAGGTGAAATCT 240

QY      367 GTAAATTTTCAATTAATAAACAACATCTACCTCCCTCTCTGTCAATCTGTGGCAGCACT 426
Db      241 GTAAATTTTCAATTAATAAACAACATCTACCTCCCTCTGTCAATCTGTGGCAGCACT 300

QY      427 TCTATATGATTTAGTATCTATATATCTGTAAGAGGTAGCGAGCGGTAAAGTAC 486
Db      301 TCTATATGATTTAGTATCTATATCTGTAAGAGGTAGCGAGCGGTAAAGTAC 360

QY      487 GGGGTTGACAGATTTTGAAGGTTGAATGATGCTTATCAAGATTAATTAATCTTCAATTA 546
Db      361 GGGGTTGACAGATTTTGAAGGTTGAATGATGCTTATCAAGATTAATTAATCTTCAATTA 420

QY      547 GAGATTTGGCTTACAGATAAATCAATCTTAAAAAATTGCTGACGTAAGTAAACAGTTC 606
Db      421 GAGATTTGGCTTACAGATAAATCAATCTTAAAAAATTGCTGACGTAAGTAAACAGTTC 480

QY      607 CAAGCAGGGAAGAGATTTCACTAACTTTAGCAGGTCATTAATCAAGAGAAAGCT 666
Db      481 CAAGCAGGGAAGAGATTTCACTAACTTTAGCAGGTCATTAATCAAGAGAAAGCT 540

QY      667 GAAATATATTTATTTGCTACGTATGTGCAAGCTGCAAAATGTGCAATTTATTAATTAAG 726
Db      541 GAAATATATTTATTTGCTACGTATGTGCAAGCTGCAAAATGTGCAATTTATTAATTAAG 600

QY      727 GAGCAGTTAAATTAATAAAGAATGGGACTAGTGTGTCACCGCTTATCAAGGCTCA 786
Db      601 GAGCAGTTAAATTAATAAAGAATGGGACTAGTGTGTCACCGCTTATCAAGGCTCA 660

QY      787 GGGAGAACTGATTTGTAACGAGCGGTTAAAGCGAAAAATAAGATTAATAATTAATTT 846
Db      661 GGGAGAACTGATTTGTAACGAGCGGTTAAAGCGAAAAATAAGATTAATAATTAATTT 720

QY      847 GTAGGTTGATTAACAAGGCTTATGATCAGATTAAGCAGCGGCTTCAAGTGTGTAAGT 906
Db      721 GTAGGTTGATTAACAAGGCTTATGATCAGATTAAGCAGCGGCTTCAAGTGTGTAAGT 780

QY      907 TGTGCTGAAATTTTAATAAATTTTGTGAGAAATGACGTTGGCGTATTTGATATTAATTT 966
Db      781 TGTGCTGAAATTTTAATAAATTTTGTGAGAAATGACGTTGGCGTATTTGATATTAATTT 840

QY      967 ATAATTTCAACTTATGATTTTGAAGAAATATCAATTAAGCAAAAGTGAAGTAACTAG 1026
Db      841 ATAATTTCAACTTATGATTTTGAAGAAATATCAATTAAGCAAAAGTGAAGTAACTAG 900
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QY      1027 GAAATTTATACAGATTCAGTGGAGATATTCAGGGGGAATATGATGGGAAACGGTTTTTT 1086
Db      901 GAAATTTATACAGATTCAGTGGAGATATTCAGGGGGAATATGATGGGAAACGGTTTTTT 960

QY      1087 AGCTTTAATTCGGTATGAAGAAATGGAACACGGGGACCTGGTTAGTACTTGCTTCA 1146
Db      961 AGCTTTAATTCGGTATGAAGAAATGGAACACGGGGACCTGGTTAGTACTTGCTTCA 1020

QY      1147 GCTATAGATATATATAGTCAATTCATTAATCTTCAAGCTTGGTATCTTAGTGGCTGGGG 1206
Db      1021 GCTATAGATATATATAGTCAATTCATTAATCTTCAAGCTTGGTATCTTAGTGGCTGGGG 1080

QY      1207 GGAATCTGCTATTAAGAGACTTCACAAAGGGTAACGGTCTTTCAACGTATGTGGA 1266
Db      1081 GGAATCTGCTATTAAGAGACTTCACAAAGGGTAACGGTCTTTCAACGTATGTGGA 1140

QY      1267 ACTACGATTAATATCACTAATATATTTTGGCAATACGATATATTTAAATTAAT 1326
Db      1141 ACTACGATTAATATCACTAATATATTTTGGCAATACGATATATTTAAATTAAT 1200

QY      1327 TCAATTAAGCTATGATGATGCAATGCAACCGTTTGTGGGATTCATTCACAGGCACTTGT 1386
Db      1201 TCAATTAAGCTATGATGATGCAATGCAACCGTTTGTGGGATTCATTCACAGGCACTTGT 1260

QY      1387 TCACTGTCAGAAATTTTTCGACAAACATAATCTTCTGTATGAGGTAAACAGTTCT 1446
Db      1261 TCACTGTCAGAAATTTTTCGACAAACATAATCTTCTGTATGAGGTAAACAGTTCT 1320

QY      1447 GGGTACTCACAGCAATTTGAATCTGTGTTACGAGTTTAATTAAGATCTTACCACTAGT 1506
Db      1321 GGGTACTCACAGCAATTTGAATCTGTGTTACGAGTTTAATTAAGATCTTACCACTAGT 1380

QY      1507 CGTACAAATTAACCTCTATAGATTAATCAAAATGCGGCAATGTGTTAAATGAACCTCCGA 1566
Db      1381 CGTACAAATTAACCTCTATAGATTAATCAAAATGCGGCAATGTGTTAAATGAACCTCCGA 1440

QY      1567 GTTAACGATTTTGGTTGACACATACAGATGAAAAAAGATATGCAATTTATCCAGAT 1626
Db      1441 GTTAACGATTTTGGTTGACACATACAGATGAAAAAAGATATGCAATTTATCCAGAT 1500

QY      1627 AAAATTAACGAAATTTCTGCAATTAAGTAAAGCTTTTGGCTTACAGCAGGTACAGATATGCA 1686
Db      1501 AAAATTAACGAAATTTCTGCAATTAAGTAAAGCTTTTGGCTTACAGCAGGTATGCA 1560

QY      1687 GGAAGTTACGTCACAGCTGGGCTGGTTATACAGAGGAGATGATTAACGTTACCTTAT 1746
Db      1561 GGAAGTTACGTCACAGCTGGGCTGGTTATACAGAGGAGATGATTAACGTTACCTTAT 1620

QY      1747 CAAGCAAGTTTAAAAATACGTTTAACTTGCACCCACGAAATTAATTAACGCTGTAGA 1806
Db      1621 CAAGCAAGTTTAAAAATACGTTTAACTTGCACCCACGAAATTAATTAACGCTGTAGA 1680

QY      1807 CTTGCTAGCGCAGTGAAGACCTGGTCCGTTCCGATGAAAGATGCTGCCAAGTTCT 1866
Db      1681 CTTGCTAGCGCAGTGAAGACCTGGTCCGTTCCGATGAAAGATGCTGCCAAGTTCT 1740

QY      1867 GTTTCAAAATGCTAATTTTCTGCTCAGGCTACAGGTCAGATGCTCATTTGATTAATG 1926
Db      1741 GTTTCAAAATGCTAATTTTCTGCTCAGGCTACAGGTCAGATGCTCATTTGATTAATG 1800

QY      1927 GACACCTTAGTATCACTAATTAATCAATGAGTGTGAATAATTAATTAACAAATCTATCT 1986
Db      1801 GACACCTTAGTATCACTAATTAATCAATGAGTGTGAATAATTAATTAACAAATCTATCT 1860

QY      1987 GGTACCACTTATTTGTGCAAAAGTGAATTTATCCCAATTAATCAATCCAAATTTGAAAA 2046
Db      1861 GGTACCACTTATTTGTGCAAAAGTGAATTTATCCCAATTAATCAATCCAAATTTGAAAA 1920

QY      2047 TGTACAAATATGTCATTTCAAGGAGACATATGATGATGAAGAGATCAATCTTGGAA 2106
Db      1921 TGTACAAATATGTCATTTCAAGGAGACATATGATGATGAAGAGATCAATCTTGGAA 1980
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Db 1621 TTTAAATATAGCTTTAACTTCTGACCCACCAATTAATTAATTCCTGTTAGACTTCGCTAC 1680
Qy 1816 GCGAGTGGAGACCTGGTCCGTTCCAGTGAAGAAAGATGTCGCCAAGTCTGTTCAAT 1875
Db 1681 GCGAGTGGAGACCTGGTCCGTTCCAGTGAAGAAAGATGTCGCCAAGTCTGTTCAAT 1740
Qy 1876 GCTAATTTTCTGCTCCAGTCAAGGCGCTATATGTTCAATTTATGAGACACTTA 1935
Db 1741 GCTAATTTTCTGCTCCAGTCAAGGCGCTATATGTTCAATTTATGAGACACTTA 1800
Qy 1936 GTTACTCATTTATCATCAATCAGGTTGAATATATTAACAATCTATCGTTACAC 1995
Db 1801 GTTACTCATTTATCATCAATCAGGTTGAATATATTAACAATCTATCGTTACAC 1860
Qy 1996 CTATTTGTTGCAAGAGTGAATTTATCCCAATTGACATCCAAATTTGAAGATGACAAA 2055
Db 1861 CTATTTGTTGCAAGAGTGAATTTATCCCAATTGACATCCAAATTTGAAGATGACAAA 1920
Qy 2056 TGTCAATTCGAGAGACATATGTATGTGAAGAGTCAATCTTGGAAACAAAAA 2115
Db 1921 TGTCAATTCGAGAGACATATGTATGTGAAGAGTCAATCTTGGAAACAAAAA 1980
Qy 2116 GAGATTGTAAATGTTATTTATTTATCAATTA 2145
Db 1981 GAGATTGTAAATGTTATTTATTTATCAATTA 2010

RESULT 4

US-10-781-979-1
; Sequence 1, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Harzels, Nadine
; APPLICANT: Harzels, Tracy
; APPLICANT: Kozlief, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5980
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-781-979-1

Query Match 39.9%; Score 855; DB 8; Length 5980;
Best Local Similarity 71.4%; Pred. No. 3e-185;
Matches 125; Conservative 0; Mismatches 430; Indels 72; Gaps 7;

Qy 8 AAATATATATTTTGTAGAAAACATTGTTACAGAAATACATTTGGGCTACTAGAAATAT 67
Db 49 AAATATATGTTATTTGTAGAAAACATTGTTACAGAAATACATTTGGGCTACTAGAAATAT 108
Qy 68 ATGAAAAGACACCTGGCATATATTTATTTAGGTGCTTTAAATTAAGACTATTAAGAG 127
Db 109 ATGAAAAGACACCTGAATATATTTATTTAGGTGCTTTAAATTAAGACTATTAAGAG 168
Qy 128 TGAATAATATGATTTCTATCAATAATCAATGAATGAATTTCTGAGATGTTCCCGA 187
Db 169 TGAATAATATGATTTCTATCAATAATCAATGAATGAATTTCTGAGATGTTCCCGA 228
Qy 188 ATTAACAATAATATGTTCAAGAGATATCTTTTGCAGAGATCCAAATATATTTCTATTA 247
Db 229 ATTAACAATAATATGTTCAAGAGATATCTTTTGCAGAGATATCTTTCTATCTATGT 288

Qy 248 ACCTGACGCTTGTGCAAGGAAAGCCATGCGAAGTACGTGGAAATCACTCGATATAG 307
Db 289 CTGGAAATGATTTCTGAGGAAATCTCATGGAGTAAATTTGGGAAATCGTGAAACGATTA 348
Qy 308 TAACTATGGGACATACCTTATCAATTTCTTGTAGAACCCGGTATATGATGAAATTCCTG 367
Db 349 CAAGTATTTGGGATTAATCTTTATGAGTTGTGTATGAAAGCTTAAGTTGGTGGAAATTA 408
Qy 368 TAAATATTTTCAATTAATTAACAAACCTATTCGTTCTTGTGCAATCTTGGACACTTT 427
Db 409 CACTATATTAATTAATTAAGAAACCTATTCGCTAATGCTCAACCTGTCTCAGCACTTT 468
Qy 428 CTATATGATTTAGTATCTATTAATTCGTAAAGAGTGAACGAGAGCGGTGAATGAC 487
Db 469 CTATATGATTTAGTATCTATTAATTCGTAAAGAGTGAACGAGAGCGGTGAATGAC 528
Qy 488 GGGTGCAGATTTTGGAGGGAATGACCTGCTATCAAGTATTAATCTTCAATATCTTG 547
Db 529 CGATTCGAGATTTTGAACGCTTAATTTGAAGAAATTTATGAGAGTATATCTTTCTATCTTG 588
Qy 548 AGGATTGGCTTACAG-----ATAATCAATCTTAATAAACTTGCTGACG 592
Db 589 GGGCTTGGCTTAAGACGTTAAACACTTCAAAAAGCAATTAATTCGATATCGAACAT 648
Qy 593 TAGTTAAACGTTCCAGACCGGAAAGAGATTTCACTAACTTTTACAGGCTCATAT 652
Db 649 TAGTTATTAATTTTAAACCTTCAGAAAGAGATTTCAATGAATTTCTAGAGGCTCATATGT 708
Qy 653 CAAGACAGAAAGCTGAATTTATTTATGCTGCTAGTATGCAAGGCGCAATGTCAT 712
Db 709 CAAGAAACAAATGCTCAAGTATTTATTTATCTTCTTGTGACAAAGCTGCAAAATGTGAGT 768
Qy 713 TATTACTATTAAGGAGCGCAGTTAAATTAATTAAGAAAGAGAGGAGCTAGTGTCCACCGT 772
Db 769 TATTACTATTAAGGAGCGCAGTTCAATTAATTAAGCAAGATGTTCCATTTTGAAGTACG 828
Qy 773 TGTATCCAGGCTCAGGAGAA-----CTGATTTGTA 802
Db 829 AGAATGTAGATCGGAATTAATTAATCACTAACAGTGGTGTGATTTTACCGGATTAATCT 888
Qy 803 AGAGAGGTTTAAAGGAAATTAAGAGATTAATTAATTTAGTGGTGTGATTAACA 862
Db 889 ATGAGGATTTAAATGCAAAACGCGAGATTAACAATTAATTTATTTATTTGATTCACG 948
Qy 863 AGGTTTATGATCAGATTAAGACAGCGCGGTACAGTCTGAAAGTTTGGTCCAAATTTAATA 922
Db 949 TAGGTTTAAATCAGATTAACAGCGGCGGACAGTGTCTGCACTTGGTCCAAATTTAATA 1008
Qy 923 AATTTGTAGAGAAATGACGTTGGCGGTATTTGATTAATTTGCTATATTTCAACTTATG 982
Db 1009 AATTTGTAGAGAAATGACGTTGGCGGTATTTGATTAATTTGCTATATTTCCAACTTATG 1068
Qy 983 ATTTGAAAATATTCATTAAGCAACAAGGTATAGTTAATCTAGGAAATTTAATACAGATC 1042
Db 1069 ATTTGAAAATATTCATTAAGCAACAAGGTATAGTTAATCTAGGAAATTTAATACAGATC 1128
Qy 1043 CAGTGGGATTTTCAAGGCGGAAATTAATGTTGGAGCGGTTT-----TTAGCTTTAAT 1096
Db 1129 CAGTGGGATTTTCAAGGCGGAAATTAATGTTGGAGCGGTTT-----TTAGCTTTAAT 1188
Qy 1097 CGGTAGAGCAATTTGAACACGCGGACCTGCTTTAGTTACTTGGCTTCAAGCTATTAAGATA 1156
Db 1189 GGTTAAGGCTATTTGAACACGCGGACCTGCTTTAGTTACTTGGCTTCAAGCAATTAAGATA 1248
Qy 1157 TATATGCTATTTATTAATCTTCACTGTTATCTGATGCTGGGCGGAGAACTGCTC 1216
Db 1249 TATATATGATTTGTT-----TCGAGATATTTTGGCGGCTGGTGAAGACTGCTC 1299
Qy 1217 ATTATGAAGCTTCACAAAGGTTAAGCGTCTTTTCAAGTATGTTGAACTTACAGATA 1276
Db 1300 ATTATGAAGCTTCACAAAGGTTAAGCGTATTTTCAAGTATGTTGAACTTACAGATA 1359
Qy 1277 ATTAATCAGTATATTTATTTTGGCAATTAACGATATATTTAAATTAATTTCAATTAGCTA 1336

Db 1360 ATGATCTAGCTATATGATTTTCAGATGCGATGTATATTAATTAATCTTCACTTAGCTA 1419
QY 1337 GATATGCAATGCAACCGTTTGTGGTATTCAATCCACGGCATCTTGTTCACGTGCAG 1396
Db 1420 ---TCATGAACTAGTAGAGAGACTAACCGCTAGACAGAGTATCGTGTTCAAAGGCAG 1476
QY 1397 AATTTTTCGACACACTAAATTAATCTTCTGTATAGAGTAACAGTCTGGG---TACT 1453
Db 1477 ATTTTGTAGGGTAGGGGGGACCTGATTTAAATTATGTGCAAGTAATATGGGCTAAGCA 1536
QY 1454 CACAGCAATTTGATCTGTGTTCACAGTATTAATGAAGTCTACACACTAGTCTGACAA 1513
Db 1537 GATGACAAATTTGATCTAGCTTCCACTTGTATGCACTAA-----TGGTATAGAG 1590
QY 1514 ATTACTCTCTAATATTTATCAATGCGGCAATGTCTTCAAAATGAACCTCCAGATTACG 1573
Db 1591 GACCTCTCATATATTAATCAATATGCGGCAATGTGTATATGGAACCTCCAGAGTTAAGC 1650
QY 1574 TATTTGGTGGACATATCAAGTATGAAAAAGTATGCAATTTATCCAGATTAATA 1633
Db 1651 TATATGTTTGGACATATCAAGTTTAAACGTGAAAAATATATTTGAAGCCAAATCAATTA 1710
QY 1634 CGCAAAATCTCGACGTAAAAAGCTTTTGCCTTACAGAGGTACAGATATGACAGAGTT 1693
Db 1711 CACAAATACCGGGGGTGAAGATTATTAATCTTCAAAATTTATCTTGTAAATGCTTATACCT 1770
QY 1694 AGCTCACAGCTGGGCT 1710
Db 1771 ATGTAAATAAAAAGCACT 1787

RESULT 5

US-10-781-979-2
; Sequence 2, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargis, Tracy
; APPLICANT: Koziele, Michael G.
; APPLICANT: Duck, Brian
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2082
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2082)
US-10-781-979-2

Query Match 34.8%; Score 747.2; DB 8; Length 2082;
Best local Similarity 69.8%; Pred. No. 9,9e-161;
Matches 1143; Conservative 0; Mismatches 433; Indels 72; Gaps 7;
QY 127 GTGAAAAATATGATTTCTTATCAAAATGAAATGAAATGAAATTTCTGATGTTCCCG 186
Db 1 GTGAAAAAGATGATCATATCAAAATTAATGAATATGAAATATGAAATCCTCATCG 60
QY 187 AATTAACCAATATGTCAACAGATATCTTTTGCAGAGGATCCAAATATATTTCTAT 246
Db 61 AATTAACCAATATGTCAACAGATATCTTTTGCAGAGGATCCAAATATATGATGATGATG 120
QY 247 AACTGAGCGCTTGTCAAGGAGGCAATGCAAGATACGTGGGAATCATGCTCGATATA 306

Db 121 TCTTGAATGATTTGCAAGGAATCTCATGGATGAAATTTGGGATTCAGTGAAGCA 180
QY 307 GTAATTTGGGACATACCTTATACAAATTTCTGTAGAACCCGATATAGTGAATTCCT 366
Db 181 ACAGATATTTGGGATTAATCTTATAGAGTTTGTATAGAACCTATAGTTGGTGAATTAAT 240
QY 367 GTAATTTTCAATTAATAACAACTCATTCGCTTCGGTCATCTGTGCACACT 426
Db 241 ACACTATATCATATATGGAATTAATTCGACTAATTCGCAACCTGTGCACACT 300
QY 427 TCTATATGATTTATGATCTATTAATTCGTAAGAGTAGACGAGAGGCTGTAAGTAC 486
Db 301 TCTATATGATTTATTTATCTATATTTGTAAGAGTAGACGAGATAGTGTTTAAGTAT 360
QY 487 GGGGTTGCAGATTTTGAAGGTAATAATGACTCTTATCAAGATTTATCTTATCTT 546
Db 361 GCGATTTGCAGATTTTGAAGGTAATAATGAAATTTATAGAGTATTTATCTTCTTATCT 420
QY 547 GAGGATTTGGCTTACG-----ATAATCAAAATCTTAATAAACTTGTCTGAC 591
Db 421 GGGGCTTGCTTAAAGACGTAACCACTTCAAAAGACAAATTAATTCGATATCGACAA 480
QY 592 GTAGTTAAACAGTTCCAGACGGAAGAGATTTCACTAACTTTTAGCAGGTCATTA 651
Db 481 TTAGTTTATATTTTAACTTTACAGAAAGATTTCAATGAATTTCTAGAGAGGTCA 540
QY 652 TCAAGACAGAAAGCTGAATATTTATTTTCTTACGTATGCAAGCTGCAATGTGAT 711
Db 541 TCAAGAAACAAATGCTCAAGTATTTGTTATTAATCTTCTTGTGCAAGAGTCAATGTG 600
QY 712 TTAATCTTATTAAGGAGCAGTTAATTAATAAAGATGGGACCTGTGTGTCACCG 771
Db 601 TTAATCTTATTAAGGAGCAGTTAATTAATAAAGATGGGACCTGTGTGTCACCG 771
QY 772 TTGTATCCAGGCTCAGGAGAA-----CTGATTTG 801
Db 661 GGAATGTAAAGATCCGAATTAATTAATCACTACAGTGTGTGATTTTACCGGTATTC 720
QY 802 AACGAGCGGTTAAACGCAAAATTAAGATTAATTAATTTGTGTAGGGTGTATAC 861
Db 721 TATGACGATTAATAATGCAAAACGCGAGATATCAATTAATTTATTTATGTATCAG 780
QY 862 AAGGTTTGAATCAGATTAAGACAGGCGGTACAAGTGTGCAAGTTTGTGCAATTTAT 921
Db 781 GTAGTTTAAATCAGATTAATAAGGCGGAGAGGTGCTGACATTTGTGCAATTTAT 840
QY 922 AATTTCTAGAGAAATGACGTTGGCGTATTTGATTAATTTCTATATTTTCAACTAT 981
Db 841 AATTTCTAGAGAAATGACGTTGGCGTATTTGATTAATTTCTATATTTTCAACTAT 900
QY 982 GATTTGAAAAATATCCATTAGCAACAGTATGAGTTAATTAAGGAAATTTATACAGT 1041
Db 901 GATTTGAAAAATATCCATTAGCAACAGTATGAGTTAATTAAGGAAATTTATACAGT 960
QY 1042 CCAGTGGGATTTCCAGGCGGAAATTAATGTTGGAACGCTTT-----TGAAGTTTAT 1095
Db 961 GCAAGTGGATTTATCCGGAATTTATGTTGTTGGAATTTGCTATATCTTTTAT 1020
QY 1096 TCGGTAGAGCAAAATGGAACAGCGGACCTGTTTATGTTATCTTGTGCTTCAACTATAGAT 1155
Db 1021 GGGTTAGAGCTATATGGAACAGCGGACCTGTTTATGTTATCTTGTGCTTCAACTATAGAT 1080
QY 1156 ATATATATGATCTTATTAATCTTCACTGTTATCTTATGAGCTGGGCGGAACCTGCT 1215
Db 1081 ATATATATGATATGTT-----TCGAATATTTTCCGGCTGGGTAGAACCTGCT 1131
QY 1216 CATTAAGAGCTTCAAGAGGTAACGCTGTTTCAACGATATGCTGGAACCTGCACT 1275
Db 1132 CATTAAGAGCTTCAAGAGGTAACGCTGTTTCAACGATATGCTGGAACCTGCACT 1191
QY 1276 AATTAATCCAGTAAATTAATTTTGTGCAATACCAATTAATTAATTTTCAATAGCT 1335

Sequence 29, Application US/10428961
Publication No. US2003023711A1
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Wei
APPLICANT: Donovan, William P.
APPLICANT: Gilmer, Amy J.
APPLICANT: Rudar, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
FILE REFERENCE: MECO201--1
CURRENT APPLICATION NUMBER: US/10/428,961
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/661,322
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.2
SEQ ID NO 29
LENGTH: 2407
TYPE: DNA
ORGANISM: Bacillus thuringiensis
US-10-428-961-29

Query Match 7.6%; Score 162.8; DB 6; Length 2407;
Best Local Similarity 53.4%; Pred. No. 1.5e-26;
Matches 434; Conservative 0; Mismatches 342; Indels 36; Gaps 3;

QY 287 GGGAAATGAGTCTGGATATATGTAATCTATGGGACATACCTTATCAATCTTCTGTAGAAC 346
DB 158 GCGATGACGAAAGAGACGATATCTATGGGACACATATGCTCTTATACACACAC 217
QY 347 CCGATATAGGTGATCTCTGATATATTTT-----CAATAATTAACAACTCATTCGT 400
DB 218 CTCTCTTACTGATTAATTTCAATATATAGTACCTTATAGTAAGTACAGAGTAA 277
QY 401 CTCTGTGATCTGTGGACGACCTTCTATATGTATTAATTAATTAATTTGTAAG 460
DB 278 GTATGACATATCATATGATATGCTATATGATTAATTAATTAATTAATTAAT 337
QY 461 AGGATGACGAGGCTTATAGTACGAGGCTTATTAATTAATTAATTAATTAATTA 520
DB 338 GGGTATGACGAGGCTTATAGTACGAGGCTTATTAATTAATTAATTAATTAAT 397
QY 521 ATCAAGATTAATTTCTTC-----ATTATCTTGAAGATTCCTTACAGATA 565
DB 398 ACAGAACTATTAAGAGCTCTGATAGTGAATTAAGATTCCTTATTCGCTTCTG 457
QY 566 AATCAATCTTAAAGAACTTGTGACGATTAACAGTTCACAGACGAGGAAAGATT 625
DB 458 AAGAACTCTGATCTGTTTAAATCGCCACCTCAGATTTGATGAATTTTAAACCG 517
QY 626 TCACATACTTTAGCAGGCTTATCAAGACGAAAGTGAATTTTATTTGCTTA 685
DB 518 GGTCTTTAAGAAATGTGCTCTGTTAGCTAGACAAATGCCCCAAATTTATTTACCT 577
QY 686 CGTATGTCAAGCTGCAATATGCTATTTATTAATTAAGGACGAGTAAATTAATAA 745
DB 578 CTTTGGAGCGCTGATTTTTCATTTATTAATTAAGGATGCTATGATATAGCA 637
QY 746 AAGATGAGGATATATGTGTCCACCGTTATCCAGGCTCAGGAGAACTGATTTAG 805
DB 638 CTATATGGGGCTATATCAATGCTACACCTTTTAA-----ATTATCAAT 682
QY 806 AGCGTTAAAGGAAATTAAGATTAATTAATTTATTTGATAGGCTGATTAACAG 865
DB 683 CAAATCTATAGCTTATTTGAATTAATTAATTTATTTGATAGGCTGATTAACAG 742
QY 866 GTTATGATGATTAAGACGAGGCTTAAAGTGTGCTGATTAATTTATTAATTAAT 925
DB 743 GTTCAACGAAATTAAGACGAGGCTTAAAGTGTGCTGATTAATTTATTAATTAAT 802

QY 926 TTGATAGAAATGACCTTGGCGGTATGATATTTATGCTATTTTCAACTTATGATT 985
DB 803 ATCGAGAGAGATGACATTTATGAGATTAAGAAATGATGATCACTTTTCAAGCTTATA 862
QY 986 TTGAAATATTCATTTGCAACAGGTGATGATTAATTAAGGAAATTTATAGATCAG 1045
DB 863 TTACTAATTTCCCAATTAAGAAAGATTTTATGATTAAGGATGATTTATTAAGATCAA 922
QY 1046 TGGATATTTCAAGGAGAAATTAATGTTGGAA 1077
DB 923 TTGATTTGTAATCTGATGATGATTTAGGGA 954

RESULT 9
US-10-929-754-4
Sequence 4, Application US/10929754
Publication No. US20050124803A1
GENERAL INFORMATION:
APPLICANT: ABDULLAH, MOHAMMAD
APPLICANT: DEAN, DONALD H.
TITLE OF INVENTION: INSECTICIDAL CRYSTAL PROTEINS WITH ENHANCED TOXICITY
FILE REFERENCE: 22727/04179
CURRENT APPLICATION NUMBER: US/10/929,754
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 60/498,826
PRIOR FILING DATE: 2003-08-29
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 4
LENGTH: 4391
TYPE: DNA
ORGANISM: Bacillus thuringiensis
US-10-929-754-4

Query Match 6.2%; Score 133.6; DB 9; Length 4391;
Best Local Similarity 48.1%; Pred. No. 1e-19;
Matches 720; Conservative 0; Mismatches 704; Indels 74; Gaps 9;

QY 666 TGAATATTAATTAATTTGCTGATGATGACGCTGCAATGTCATTTATTAATTAAG 725
DB 1303 TGAGTATCTTTATTTGCTGCTCTATGACAAATTTGCAATTCGATTTATTTAG 1362
QY 726 GAGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 785
DB 1363 GATGCTCAGATTTATGAGATTAATTAATTAATTAATTAATTAATTAATTAAT 1407
QY 786 AGGAACTGATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 845
DB 1408 TGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1467
QY 846 TGTAGGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 905
DB 1468 TATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1516
QY 906 TTGCTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 965
DB 1517 -TGGTAACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1575
QY 966 TATATTTCACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1025
DB 1576 AATGTTCCCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1635
QY 1026 GGAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1085
DB 1636 GGAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1692
QY 1086 TACCTTAATTTGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1145
DB 1693 TTCTTTGGAAGGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1752
QY 1146 AGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1205
DB 1753 AGGATTTGATTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1812

QY	1206	GGGAACCTCGTATTATGAAGCTTCACAAAGGTAAACGGTCTTTTCCAAAGTATGCTGG	1265
Dp	1813	TAAGTATTCTTATCTAATAATTTCTAGATTAAAGAGGGCTTTTAAAGGACAGAC	1872
QY	1266	AACACAGATATATATCCAGTAATATTTT---GGCAATACGATATATTTAAAT	1322
Dp	1873	AGATTATAGTGGACCTCTTCTACCACTTAATTTCCATCAAAATTCGATGATATTAATTT	1932
QY	1323	TATTTCAATYAGCTAGATATGCAATGCAACGTTGTTGGATTTCA--ATCCACGGCA	1379
Dp	1933	ATGACGGAAATATATGAAATATTTATCCCTTGGGGTATCCCTGTAATATATTAACAAAAT	1992
QY	1380	TCCTGTTTTCACGTCAGAAATTTTTTCCGACAACACTAAATATCTTCCGTATGAGTTAA	1439
Dp	1993	GAATTTTCTGTACACAGTAAATATTTCTTCAAAAAGATTAATTTATGTTGCACACAGAC	2052
QY	1440	CAGTTCTGGGTACTCACAGACAATTTGAATCTGTGTACAGATATTAATAGATTTAC	1499
Dp	2053	GAATTAACCTGTGTGGACAGATTTTGATTTCTCACTAATTAAGGGACGTAGTT	2112
QY	1500	ACCTAATCGTACAAATTTACTCTCATATTTATCAATGCGGACGTGTTCAAA-----	1553
Dp	2113	AGCAAAATATATGATATATATCAATATTTTATCTATATGTTAATATATGCGGAAACGTT	2172
QY	1554	---TGAACCTCCAGAGTTAACGATTTGGTTGGACATACATCAAGTATGAAAAAGATTA	1610
Dp	2173	TGCTCAGAAACGTATGTTATGCTTTTACACATATGATGTGTGATCTTAATTA	2232
QY	1611	TCGAATTTATCCAGATAAATTTAAGCAAAATTCCTGCAGTAAACGTTTGGCCCTACAGC	1670
Dp	2233	TACCATTCGACGATATAAATTTAGCAAAATTCCTGTAGTGAAGGTTGGAATATAATG	2292
QY	1671	AGATACAGATATGCAAGAGTTACGTACACAGCTGGGCTGTGTATACAGAGAGATGT	1730
Dp	2293	ATCGATTTCAATGAAAAAGT-----CCCGAATTTACGGAGAGAGATTT	2337
QY	1731	AGTAAAGTTACTTATCAAGCAAGTTTAAAAATAGTTTAACTTCTGCAGCCACGAGATTA	1790
Dp	2338	GGTAAAGATGAGACAGATTAAGGTTTAACTATAGCGTTTAAAGCTGAATTTATAGATTA	2397
QY	1791	AAATTAACCGTTAGACTTCGCTACGCGAGTGAAGGACCTGTCGCTCCGAGTAGAAAG	1850
Dp	2398	AAATATATGTTGTGAATAGCTTTAATATGTAATGTAACAGTTCTTAATTAATACAGAA	2457
QY	1851	ATGG---TCGCAAGTTCTGTTCAATGCTAATTTTCTGTCACGCTACAGGTGCTA	1907
Dp	2458	ATGGAAGGGAGAGTTATATACAAACAACAAATTCACAATTTTCTCCCATATGAGGC	2517
QY	1908	TAGTTCAATTTGATTATATGAGCAACCTTAGTTACTATCAATTTATCAATAGGTTTGAAT	1967
Dp	2518	CTTTTCTTATTTAGAGTCTTTTAACTAATCTACGACACAAAAATATATTTGATTTGACAT	2577
QY	1968	AATTATACAAATCTATCTGTGTACACCTTATGTTGACAAAGTCGATTTATCCCAAT	2027
Dp	2578	GGAGGTAAACATATCCGTATGTAAGACATTTGTTGAAGATATACATCTCTTAATTTAGA	2637
QY	2028	TGACATCCAAATTGAAAAATGTAGCAAAATGTCAATTCGAAGAGACATATGTAGATGTGA	2087
Dp	2638	TAAATATGAATTTCTCCCACTAATCGATTAACATTCACA-----GGAATATATGA	2686
QY	2088	AGGAGTACAAATCTTTGGAACAAAAAAGAGATGTAAATGATTTATTTATCAATTTAA	2145
Dp	2687	GGAAAAATATGATTTGAAAGATCCAGGAAACATTTAATATGTAATTTGTTGATTTAA	2744

RESULT 10
US-10-428-961-5
; Sequence 5, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Wei

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1  APPLICANT: Donovan, William F.
2  APPLICANT: Gilmer, Amy J.
3  APPLICANT: Rudat, Mark J.
4  TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
5  TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
6  FILE REFERENCE: MEC0201-1
7  CURRENT APPLICATION NUMBER: US/10/428,961
8  CURRENT FILING DATE: 2003-05-02
9  PRIOR APPLICATION NUMBER: 09/661,322
10 PRIOR FILING DATE: 2000-09-13
11 PRIOR APPLICATION NUMBER: 60/153,995
12 PRIOR FILING DATE: 1999-09-15
13 NUMBER OF SEQ ID NOS: 63
14 SOFTWARE: Patentin version 3.2
15 SEQ ID NO 5
16 LENGTH: 1959
17 TYPE: DNA
18 ORGANISM: Bacillus thuringiensis
19 US-10-428-961-5

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Query Match	5.6%;	Score 119.8;	DB 6;	Length 1959;
Best Local Similarity	55.0%;	Pred. No. 1e-16;		
Matches 294; Conservative	0;	Mismatches 217;	Indels 24;	Gaps 2

Qy	56	AGATTAATCAAAATCCATAAAAAACCTTGCTGACGTGTGTTAAACAGTTCACAGACGGGAGAGA	620
Db	411	AGATTAACCGAAATGATGTCAMAGATCAAGAACATATTATTCTTGAGGCGCTATGTGCTTTAGA	470
Qy	621	AGATTTCACITAACTTTTACGAGGGTCATTATCAAGACAGAAAGCTGAATATTATTATT	680
Db	471	ACTTGACATTATCTACCTGCTATACCGCTTTTCAGAAATGCAAAATGMAAGTTCATTATT	530
Qy	681	GCCCTACGTATGTGCAMCTGCAAAATGTGCATTTTATCTATTATTAAGGACGCAGCTTAAATA	740
Db	531	AATGTATATATGCTACAGCTGCAAATTTACACCTATATTATTGTAGAGACGATCCCTTTT	590
Qy	741	TAAAAAAGAAATGGGGACTAGTGTCTCACCGTTGTATCCAGGGTCAGGGAGAACTGAATTG	800
Db	591	TGTATGTAAATGGGGGATGGCATCTTCGCATGTGTAAACAA-----TA	632
Qy	801	TAAAGACGCGGTAAAAACGAAAAATAAAAAGATTACTAATTAATTGTGAGGGGTGTATTA	860
Db	633	TTACACAGAAACAAATCAGATATACAGAGGAATATCTTACACATTTGCGTACATGTATTA	692
Qy	861	CAAGGTTTAAATCAGATTAAGACAGCGGGTACAAAGTCTGAAGTTTGGTGCAAATTTAA	920
Db	693	TACAGGGCTTAAATTAACCTTAAGA-----GGACCAAAATGCTGAAGTGTGGTCCGTATTA	746
Qy	921	TAAATTTGTAAGAAATGACGTTGGGCGGTATTTGGATATTAATTCGCTATTTCCAACTTA	980
Db	747	TCAATTTCCGTAGAACCTTAAGGTTTGGGGGTATTTAGATTAGTACGCTATTCCCAAGCTA	806
Qy	981	TGATTTTGA AAAAATATCCATTAGCAACAGGTAGAGTTTAACTTAGGAAATTTTATACAGA	1040
Db	807	TGATATCTGCACCTATCCATCAATTAAGAGTCTCAGTTTAAACAAGAAATTTTATACAGA	866
Qy	1041	TTCAGTGGGAATTTCAAGGGGAAATTAATGTGTGGGAACGTTTTTATGCTTTAAT	1095
Db	867	TTCAATATGGGAGAAACAATGCACTTACAGGATTTTGCAGATTCGAATGTGTTTTAAT	921

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RESULT 11
US-10-782-020-4
; Sequence 4, Application US/10782020
; Publication No. US2004019791CA1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXM1-004, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use

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; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782.020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1806
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1806)
US-10-782-020-4

Query Match      5.5%; Score 117.6; DB 8; Length 1806;
Best Local Similarity 46.6%; Pred. No. 3.1e-16;
Matches 535; Conservative 0; Mismatches 589; Indels 24; Gaps 4;

QY 532 TATCTTCATTATCTTGAGATTGGCTTACAGATAATCAATCCTAATAAACTTGCTGAC 591
DB 310 TATATACAAATTACGTAATGGAATGGAATAATGATATGMAAACTCAAGGCTCAAGGTAG 369
QY 592 GTAGTTAAACAGTCCACAGACGGGAAGATTTCCTAACTTTAGCAGGGTCAATTA 651
DB 370 GTAGCTAATTACTATGAAAGCTTTGACAGCGGCTGMAAGAGTATGCC---TCAATTT 426
QY 652 TCAAGACAGAAAGCTGAATATTTATTTGCTACGTATGCAAGCTGCAAAATGTCAT 711
DB 427 GCAGTGAAGAAATTTGGAATGCCACTTTTAATCTCTATGTGCAAGCTGCTAATCTTCAT 486
QY 712 TTAATTACTATTAAGGAGCGAGTAATTAATTAATAAAGATGGGACTAGTGTCCACCG 771
DB 487 TTAATTATTTAAGAGATGTTTACGTTTATGMAAGTGTGGGA----- 531
QY 772 TTGTATCCAGGTCAGGAGAACTGATTGTACAGAGCGGTTAAAGCGAAATTAAGAG 831
DB 532 TGGTCGAGACAGAAATTAATAATTTATATGATTAACAGATTA---GTATACCCATGAA 588
QY 832 TATACTAATTAATGTGAGGAGTGTATTAACAGGCTTTAGTCAATGATTAAGACGGGGT 891
DB 589 TACACAAATCATCTGTGTAATTTGATATTAAGAGACTTGAAGATTTAAATAAAGGT 648
QY 892 ACAAGTCTGAAGTTTGTGCAAAATTAATTAATTTGTGAGAGAAATGACGTTGGCGTA 951
DB 649 TCTTCTATCAAGATTGTAATTAATTAATTAATTCGTTCCGTGAGAAATGACCTTACGTT 708
QY 952 TTGATATTAATGTGTAATTTCCACTTAATGATTTTGAATAATTCATTAGCAACAAGT 1011
DB 709 TTAGATATTCGTGCTTATTTCCCGCACTATGATGTACAACTTATCCATTAACAAACGTT 768
QY 1012 GTAGAGTTAACTGAGGAATTTTATACAGATCCAGTGGGATTTCAAGGGGGAAT---AT 1068
DB 769 GCTCAGCTTAACAGGAAGTTTATACGATCTTTTACTTAATTTTAAATCCTTAATTAATCAT 828
QY 1069 GGTGGGAAGCGTTTTTTAGCTTTAATTCGTGAGAACCAATGGAACACCGGGAACCTGTG 1128
DB 829 TCTGTGTCTCAATTAAGTTTATAGTACATGGAATAAATGCAACAATTAACACCTCCAT 888
QY 1129 TTAGTTACTGCTTCAAGCTATGATATTAATTAATTAATTAATTTTCAAGCTTGGT 1188
DB 889 CTATGGAATTTTAAAGATGCTAAACAATTAATTAACAGATTGTATAGTGTGGGAAGAAC 948
QY 1189 TATCTTAGTGGCTGGGGGGAACCTGCTATTATGAACCTTCAAGGGGTAACGGTCT 1248
DB 949 TATATATGGGGAAGACATCGCGTGAAGCTTTACATGTAGAGAGAGATATTAAGTCA 1008
QY 1249 TTTCAAGCTATGTCTGAACTACAGATTAATTAATTCACGTAATTAATTTTGGCAATACC 1308
DB 1009 CCTCTATATGTAGAGAGGCAAAATCAAGAGGTTCTGTAGAGATTTTATTTTATGAGACC 1068
QY 1309 GATATATTTAAATTTATTTGATTAGCTAGATATGCAATGCAACCGTTTGTGGGTATTC 1368

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DB 1069 GTTTTAAAGCTTATTCMAAGCGACTTAAGACCATTAACAGACCTGACCAAGCTCT 1128
QY 1369 ATCCACGGCATCTTGTGTTACGTGACGAAATTTTTCGCAACAACATAATTAATCTTCTG 1428
DB 1129 CCTTTAATTTAGTACTTATGAGGAGTGAATTCACACTCTTACAGAGTATGTTATG 1188
QY 1429 TATGAGTAAACAGTTCTGGGTACTCAACAGCAATGAATCTGTGTTACAGAGTATTAAT 1488
DB 1189 TATCGTGAAGAGATCGGTAGATTTCTTTAATGAGTGGCGCTTTAATCCAGTTGGG 1248
QY 1489 AAGATCTACCACTTACTGTCTACAAATTAATCTCATATGATTAATCAAAATGGGATGTT 1548
DB 1249 TTAACCTTAAGATTAACATCAACCTGTTATGTATGCAACGTTTGTGTAATATCGGG 1308
QY 1549 CAAATGAACCTCCAGAGTTAAGCTATTTGTTGGACATATCAAGTATGAATAAAGAT 1608
DB 1309 ACCCTTTATTTAAACACAGGTGCCATCTTTCTTGGACACATGTAGTCTGAAGAAC 1368
QY 1609 AATGCAATTTATCCAGATAAATAATTAACGCAATTCGTGACGTAAAGCTTTTGCCCTA 1668
DB 1369 AATACAAATGAATCAATATTTATTAACGCAATCCCGTTAGTAAAGCATATCAAAATGGG 1428
QY 1669 GCAGGTAC 1676
DB 1429 TCAGGCAC 1436

RESULT 12
US-10-782-020-2
; Sequence 2, Application US/10782020
; Publication No. US20040197916A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: Axmi-004, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782.020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1890
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1890)
US-10-782-020-2

Query Match      5.5%; Score 117.6; DB 8; Length 1890;
Best Local Similarity 46.6%; Pred. No. 3.2e-16;
Matches 535; Conservative 0; Mismatches 589; Indels 24; Gaps 4;

QY 532 TATCTTCATTATCTTGAGATTGGCTTACAGATAATCAATCCTAATAAACTTGCTGAC 591
DB 394 TATATCAATTAATCGTATATGAATGGAATAATGATATGMAAACTCAAGGCTCAAGGTAG 453
QY 592 GTAGTTAAACAGTCCACAGACGGGAAGATTTCCTAACTTTAGCAGGGTCAATTA 651
DB 454 GTAGCTAATTACTATGAAGACTCTTGAGCAGCGGCTGAAAGAGTATGCC---TCAATTT 510
QY 652 TCAAGACAGAAAGCTGAATAATTAATTTATTTGCTTACGTATGTGCAACCTGCAATGTGCAT 711
DB 511 GCAGTGAAGAAATTTGAAATGACACTTTTAACGTCTATGTGCAACCTGTAATCTTCAT 570
QY 712 TTAATTACTATTAAGGACGCAATTAATTAATAAAGATGGGACTAGTGTCCACCG 771

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Db 571 TTTATTTATTTAGAGATGTTTCAGTTTATGAAAGTTGGGA----- 615
QY 772 TTGTATCCAGGCTCAGGAGAACTGATTTGAACAGCGGTTAAAGCGAAATTAAGAG 831
Db 616 TGGTCGAGAGCAAAAATTAAATTTTATGATTAACAGATTAA---GATATCCCATGAA 672
QY 832 TATCTAATTAATTTGTAGGGGTGTATTAACAGAGGTTTAGATCAGATTAAGACAGCGGGT 891
Db 673 TACACAATCATTTGTGTAATTTGATATTAAGAGCTTAGAGATTTAAAAATTAAGGT 732
QY 892 ACAAGTCTGAAGTTTGTGCGAAATTTAATMAATTTGTAAGAGAAATGACGTTGGCGTA 951
Db 733 TCTTCTTATCAAGATTTGTATCAATTAATATGTTTCCGTAGAGAAATGACTTACTGTT 792
QY 952 TTGGATTTATTTCTATATTTCCACTATGATTTTGAATAATTCATTAGCAACAGT 1011
Db 793 TTAGATATCGTTCTTATTTCCGCACTATGATGTACAACTTATCCAAATMACACCGTT 852
QY 1012 GTAGATTAATCTAGGAAATTTTATACAGATCCAGTGGATATTCAAGGGAATTT---AT 1068
Db 853 GCTCAGCTAACAGAGAAAGTTTATACGATCTTTACTTATTTTATCTTAATTTACAT 912
QY 1069 GGTGGGAACGTTTTTTAGCTTTAATTCGTAGAAAGCAAAATGGAACAGGGAACCTGGT 1128
Db 913 TCTGTCTCAATTAATCTAGTTTATAGTATGATGAAATGCAACAAATTAGAACTCCACAT 972
QY 1129 TTATTTACTTGGCTTCAAGCTATAGATATATATATGTCATTCTTATTACTTCAAGCTTGT 1188
Db 973 CTATGGAATTTTAAAGATGCTAACATTTTATACAGATTGTATGTTGGAGAAAGAC 1032
QY 1189 TATCTTAGTGGCTGGGGGGAACCTGCTATTATGAAGACTTCAAAAGGTTAAACGGTGT 1248
Db 1033 TATTTATGGGAGAGACATGCGTGAAGCTTTACATGTAGAGAGAGAAATTAAGATCA 1092
QY 1249 TTTCAACGTAATGCTGGAATACGAGTAATTAATCAAGTAATTTATTTTGGCAATACC 1308
Db 1093 CCTCTATATGTAGAGAGCAAAATCAAGAGGTTCTTAGAGATTTTATTTTATGAGACC 1152
QY 1309 GATATATTTAAATTTATTTCAATTAAGTATGATGATGCAACCGTTTGTGGGATATCA 1368
Db 1153 GTTTTAAAGCGTTATCAAGCCGATCTTAAGACATTTACAGACGCTGACACAGCTCCT 1212
QY 1369 ATCCACGCGCATCTTGTTCACGTCAGATTTTTCGCAACAACATAATTTACTTCTCTG 1428
Db 1213 CCTTTAATTTAGTATGCTTAGAGAGATGAATTTCAACCTCTACAGGATTTTATG 1272
QY 1429 TATGAGTAAACAGTTCTGGTACTCACAGCAATGGAATCTGTGTTTCCAGGTAATTAAT 1488
Db 1273 TATCGTGAAGAGATCGTAGATTTCTTTAATGAGTTGCGGCTTTAATCCAGTTGGG 1332
QY 1489 AAGATCTACACCTAGTCTGACAAATTAATCTCATGATTTATCAAAATGGCGCATGTT 1548
Db 1333 TTAACCTATAGGTATACAGTCAACGTTTATGTCATCAACGTTTGTTCGTAATCTGGG 1392
QY 1549 CAATAATGAACCTCCAGATTTAAGTATTTGTTGACACATCAAGATATGAAGAAAGAT 1608
Db 1393 ACCCTTATTTAACAACAGGTGCATCTTTCTTGACACATGTAATGCTGAAGAAACC 1452
QY 1609 AATGCAATTTATCCAGATTAATTAATGCAAAATTCCTGACAGTAAAGCTTTTGCCTTACA 1668
Db 1453 AATACATTTGAATCAATTAATTAATGCAAAATCCGTTAGTAAAGATATCAAAATTTGGG 1512
QY 1669 GCAGGTAC 1676
Db 1513 TCAGGCAC 1520
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RESULT 13

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US-10-782-020-1
; Sequence 1, Application US/10782020
; Publication No. US20040197916A1
; GENERAL INFORMATION:
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; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargis, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782,020
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2190
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-782-020-1

Query Match      5.5%; Score 117.6; DB 8; Length 2190;
Best Local Similarity 46.6%; Pred. No. 3.4e-16;
Matches 555; Conservative 0; Mismatches 589; Indels 24; Gaps 4;

QY 532 TATCTTCAATTAATCTGAGATTTGCTTACAGATTAATCAATCTTAAACTTGTCTGAC 591
Db 694 TATATCAATTAATGATATGATGAGAAATGATATTTGAAAATCAAAAGCTCAAGGTAAAG 753
QY 592 GTATGTTAAACAGTTCCAGACAGGAGAGAAATTTCACTAACTTTAGCAGGTCATTA 651
Db 754 GTAGCTAATTAATCAAGAAATCTTGGAGCGGCTTGAAGAGATATGCC---TCATTT 810
QY 652 TCAAGCAGAAAGCTGAATATTTATTTGCTTACAGTATGTCAGAGCTGAATGTCAT 711
Db 811 GCAGTGAAGAAATTTGAAGTACACTTTTAACTGCTTATGTCAGAGCTGTAATCTTCAAT 870
QY 712 TTATTTACTTAAAGGACGCAAGTAAATTAATTAAGAAATGGGGACTAGTGTGTCCACCG 771
Db 871 TTTATTTATTTAAGAGATGTTTCACTTATTAAGAAAGTGTGGGA----- 915
QY 772 TTGTATCAAGGCTCAGGGAACCTGATTTGAACGAGCGTTAAAGCGAAATTAAGAG 831
Db 916 TGGTCGAGACAGAAATTTAAATTTATATGATTAACAAATTA---GTAATCCCATGAA 972
QY 832 TATCTAATTTATTTGTCAGGTCAGTATTAACAGGTTTATGATCAAGTAAAGAGCGGCT 891
Db 973 TACACAATTCATTTGTATTAATTTGTAATTAAGAGCTTAGAGATTTAAATTAAGGT 1032
QY 892 ACAAGTCTGAAGTTTGTGCGAAATTTAATTAATTTCTGAGAGAAATGACGTTGGCGGTA 951
Db 1033 TCTTCTTATCAAGATTTGTATCAATTTATATCGTTTCCGTAGAGAAATGACTTACTGTT 1092
QY 952 TTGGATTTATTTGCTATATTTTCCAACTTATGATTTTGAATAATTCATTAGCAACAGT 1011
Db 1093 TTAGATATCGTTGCTTATTTCCGCACTATGATGTAACAACTTATCAATCAACCGTT 1152
QY 1012 GTAGATTAATCTAGGAAATTTTATACAGATCCAGTGGGATTTTCCAGGGGAATTT---AT 1068
Db 1153 GCTCAGCTAACAGGAAAGTTTATACGATCTTTTACTTAATTTTATCTTAATTAATCAAT 1212
QY 1069 GGTGGGAACGTTTTTTTGTGCTTTAATTCGATGAGAGCAAAATGGAACAGGGAACCTGGT 1128
Db 1213 TCTGTCTCAATTTACTTACTTGTATGACATGAGAAAATGCAACATTTGAACTCCACAT 1272
QY 1129 TTAGTTACTTGGCTTCAAGCTATAGATATATATGATTAATGCTTATTAATCTTCACTTGGT 1188
Db 1273 CTGATGGAATTTTAAAGATGCTTAACAAATTTATACAGATTTGATATGTTGGAGAAAGAC 1332
QY 1189 TATCTTAGTGGCTGGGGGGAACCTGCTATATGAAGACTTTCACAAAGGTTAACGTTGCT 1248
Db 1333 TATTTATGGGAGAGACATGCGGTGACGTCCTTACCAATGATGAGAGAGAAATTAAGATCA 1392
QY 1249 TTTCAACGTAATGCTGGAACCTAGAGTAATTAATCCAGTAATTAATTTTGGCAATACC 1308
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Db 1393 CCTATATAGTGAAGAGGCAATCAAGAGGTTCTTGAAGATTTTATTTTATGACCC 1452
QY 1309 GATATATTTTAAATTTATTTATTTAGTATGATGCAATGCAACGTTTGTGGATATTC 1368
Db 1453 GTTTTAAAGAGGTTATCAAGCCGACTTAAGACATTAAGCAGCCGACAGCTCCT 1512
QY 1369 ATCCAGGCAATCTTGTTCACGCGCAAAATTTTTCGACACACTAAATACCTTCCTG 1428
Db 1513 CTTTAAATTTTACGTTAGAGGAGTGAATTTTCACTCTTACAGGATGTTTATG 1572
QY 1429 TATGAGTAAACAGTCTGGGTACTCAAGCAATGATGATGCTGATACAGATTAAT 1488
Db 1573 TATGTTAAAGAGATGATGATGATTTCTTTATAGATGTCGCTTTTAAATCCAGTGG 1632
QY 1489 AAGATCTACCACTAGTCTGATCAATTAATCTGATGATTAATCAATGCGGATGTT 1548
Db 1633 TTACCTCATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1692
QY 1549 CAAATGAAACCTTCAAGATTAACGTAATTTGTTGCAACATACAGATGATGAAAAAG 1608
Db 1693 ACCCTTATTTTAAACAGAGGCGCATCTTTCTTGACACATCGTATGCTGAAGAAC 1752
QY 1609 AATGATTTATTCAGATTAATTAAGCAATTCCTGAGTAAAGCTTTTGCCTACCA 1668
Db 1753 AATGATTTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1812
QY 1669 GCAGGTAC 1676
Db 1813 TCAGGCAC 1820
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RESULT 14

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US-10-428-961-62
; Sequence 62, Application US/10428961
; Publication No. US2003023711A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rel
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rudat, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 3684
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-428-961-62
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Query Match 5.4%; Score 116.8; DB 6; Length 3684;

Best Local Similarity 55.0%; Pred. No. 6,7e-16; Matches 310; Conservative 0; Mismatches 227; Indels 27; Gaps 3;

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QY 532 TATCTTATATATCTTGAAGATGCTTACAGATTAATCAATCTTAAATCTTAAATCTTGCAC 591
Db 400 TATCAACAGTCACTGAAGATTTGGCTGAGAAACCGTATGATGCAAGAGAGAGTGT 459
QY 592 GTAGTTAAAGTTCACAGCAGGAGAAAGATTTCACTAACTTTTGAAGAGGTCATTA 651
Db 460 CTTTATACCAAAATATATAGCTTAGAATTTCTTATGATGAGAGCCGCTTTTCGCA 519
QY 652 TCAAGACAGAAAGTGAATATTTATTTGCTGATGATGCAAGTGAAGTGAATGTCAT 711
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Db 520 ATTGAACCAAGAGTTCATTTATATG---GTATATGCTCAAGCTGCAATTTACAC 576
QY 712 TTAATTAATTAAGGACGAGTAAATATATTAATTAATTAATTAATTAATTAATTAATTA 771
Db 577 CTATATATTAATGAGATGCTCTCTTTTGTATGTAATTTGGGCTTATATCCAGAA 636
QY 772 TTGATTCAGAGGTCAAGGAGAACTGATTTGTAAGAGCGGTTAAAGCAATTAATTAAG 831
Db 637 ATTCACG-----TTATATGAGGCCAAGTGTGAAAAACAGAGAA 678
QY 832 TATCTAATTAATTTGTAGGAGGTGTATTAACAAGGTTTATGATGATTAACAAGCGCGGT 891
Db 679 TATCTGATTAATTTGCGCAAGATGATTAATTAACGGGTTTAAATTAATTAATTAATTA 732
QY 892 ACAAGTCTGAAGTTTGTGCGAATTAATTAATTAATTTGATGAGAAATGACGTTGGCGTA 951
Db 733 ACAATGCTGAAGTTGTTGTTGCGATTAATTAATTAATTTGATGAGAAATGACGTTAGAG 792
QY 952 TTGATTAATTTGCTATATTTTCCACTTATGATTTGAAAAATATTCATTTAGCAACAGT 1011
Db 793 TTGATCTAGTGGACACTATTTCCAGCTATGACACGCGTGTATTCATGAAATACAGT 852
QY 1012 GTAGATTAATCTAGGAAATTTATACAGATCCAGTGGATATTCAGGCGGAATTAATGT 1071
Db 853 GCTCAATTAACAAGAGAAATTTATACAGATCAATTTGGAGAAACAATGACCTTCAGGA 912
QY 1072 TGGAAACGTTTATTTAGCTTTAAT 1095
Db 913 TTGCAAGTACGAATTTGTTTAAAT 936
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RESULT 15

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US-10-665-460A-7
; Sequence 7, Application US/10665460A
; Publication No. US20040096934A1
; GENERAL INFORMATION:
; APPLICANT: Freysinet, Georges
; APPLICANT: Rang, Cecile
; APPLICANT: Futos, Roger
; TITLE OF INVENTION: Pepsin-sensitive modified Bacillus thuringiensis insecticidal
; FILE REFERENCE: A35992-PCT-USA-A (072667.0191)
; CURRENT APPLICATION NUMBER: US/10/665,460A
; PRIOR FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: PCT/FR02/00772
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: FR 01/03691
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Artificial sequence description: Cry9Ca1 Glu-164
; NAME/KEY: CDS
; LOCATION: (1)..(2019)
US-10-665-460A-7
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Query Match 5.3%; Score 113.4; DB 7; Length 2019;

Best Local Similarity 55.8%; Pred. No. 3e-15; Matches 294; Conservative 0; Mismatches 206; Indels 27; Gaps 3;

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QY 527 ATTATATCTTATTTCTTGTAGAGATTTGGCTTACATTAATTAATTAATTAATTAAT 586
Db 440 ATGTATATCAACGTTCCCTTCAAAATTTGTTGCTGATGAAATGATTAACGAAATTTTA 499
QY 587 CTGACGTAGTAAACGTTCCCAAGCAGGAGAAAGATTTCACTAACTTTTGAAGAGGT 646
Db 500 GTCTTGTCTGTCTCAATTTATAGCTTTAGACCTTGAATTTTGTATATGCTATTC---T 556
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QY	647	CATTATCAAGACAGAAACCTGAAAATATATATATATGCTCAAGATATGCAACTGCAATG	706
Db	557	TGTTTGCAGTAAATGAGACAGAGTTCCATTACTGTCAGTATATGACAAAGCTGTGAATT	616
QY	707	TGCATTATATCTATTTAAGGACGCGATTTAAATATATAAAAAAGATGGGAGACTAGTGCTC	766
Db	617	TACATTGTATTTATTTAAAGATGTCATCTTTTGGAGAAAGATGGGATTC-----	670
QY	767	CACCGTGTATCCAGGGTCAGGGAGAACTGATTTGTAACGACCGGTTAAAGCGAAAAATTA	826
Db	671	-----CACAGGGGAAAAATTTCCACATATTTATGACCGTCAATTGAACTTAACCG	718
QY	827	AAGATATACTAATTAATTTGTGTAGGGGTGTATTAACAAGGTTTAGATCAGATAGACAG	886
Db	719	CTAAGTACACTAATTACTGTGAAACTTGTATATACAGGTTTAGATCGTTTAAAGA-----	774
QY	887	CGGGTACAAGTGTCTGAAGTTTGTCGAAATTTAATTAATTTTCGTAGAGAAATGACGTTGG	946
Db	775	--GGAAACAAATACGNAAGTTGGTTTAAATATCATCAATTCGTTGAGAAATGACTTAA	832
QY	947	CGGTATTTGGATATTTATGCTATATTTCCACTATGATTTTGGAAAAATATCATTTAGCA	1006
Db	833	TGTATTTAGATGTTGTGGCGCTATTTCCATATTAAGAGTATACGACTTTATCCACAGGAT	892
QY	1007	CAGGTGTAGATTAACTAGGNAATTTTATACAGATCCAGTGGGAAT	1053
Db	893	CAAAACCAAGCTTACAGTGAAGGTATATACAGATCCAGTGTGATTT	939

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Job time : 1174.77 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:27:04 ; Search time 267.352 Seconds

(Without alignments)
14261.593 Million cell updates/sec

Title: US-10-782-141-1

Perfect score: 2145
Sequence: 1 ttccaccaataataacgttc.....atagttattatcaattaa 2145

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172.4	8.0	3468	3	US-09-001-982-9
2	172.4	8.0	3468	3	US-09-668-650-9
3	172.4	8.0	3471	3	US-09-002-285-71
4	172.4	8.0	3471	3	US-09-589-477-71
5	172.4	8.0	3471	3	US-10-099-285A-71
6	172.4	8.0	3726	3	US-09-001-982-11
7	172.4	8.0	3726	3	US-09-668-650-11
8	162.8	7.6	2407	3	US-09-661-322A-29
9	119.8	5.6	1959	3	US-08-100-709-3
10	118.2	5.5	3934	2	US-08-176-865-3
11	118.2	5.5	3934	2	US-08-474-038-3
12	118.2	5.5	3934	2	US-08-779-046-3
13	118.2	5.5	3934	2	US-08-881-340-3
14	116.8	5.4	3684	2	US-08-448-170-7
15	116.8	5.4	3684	2	US-08-961-803-5
16	116.8	5.4	3684	3	US-09-661-322A-62
17	112.4	5.2	4173	3	US-09-661-322A-37
18	111.8	5.2	1897	3	US-09-363-970-5
19	111.8	5.2	3471	3	US-09-002-285-73
20	111.8	5.2	3471	3	US-09-589-477-73
21	111.8	5.2	3471	3	US-09-661-322A-27
22	111.8	5.2	3471	3	US-10-099-285A-73
23	111.8	5.2	4344	2	US-08-532-547-4
24	111.8	5.2	4344	2	US-08-532-547-4

25	111.8	5.2	4344	2	US-08-379-656B-4	Sequence 4, Appl1
26	111.8	5.2	4344	3	US-08-455-838-4	Sequence 4, Appl1
27	111.8	5.2	4344	3	US-09-019-809-4	Sequence 4, Appl1
28	111.8	5.2	4344	3	US-09-471-177-4	Sequence 4, Appl1
29	111.8	5.2	4344	3	US-09-220-806-4	Sequence 2, Appl1
30	110.8	5.2	1561	2	US-08-532-547-2	Sequence 2, Appl1
31	110.8	5.2	1561	2	US-08-379-656B-2	Sequence 2, Appl1
32	110.8	5.2	1561	3	US-08-455-838-2	Sequence 2, Appl1
33	110.8	5.2	1561	3	US-09-019-809-2	Sequence 2, Appl1
34	110.8	5.2	1561	3	US-09-471-177-2	Sequence 2, Appl1
35	110.8	5.2	1561	3	US-09-220-806-2	Sequence 2, Appl1
36	107.8	5.0	1607	3	US-08-286-870A-5	Sequence 5, Appl1
37	107.8	5.0	1946	3	US-08-286-870A-3	Sequence 3, Appl1
38	107.8	5.0	2965	2	US-08-460-570-1	Sequence 1, Appl1
39	107.8	5.0	2965	2	US-08-460-570-2	Sequence 1, Appl1
40	107.8	5.0	2965	3	US-08-286-870A-1	Sequence 1, Appl1
41	107.8	5.0	2965	3	US-08-286-870A-2	Sequence 2, Appl1
42	105.2	4.9	3507	2	US-08-315-468-3	Sequence 3, Appl1
43	104.4	4.9	4074	2	US-08-377-690-1	Sequence 1, Appl1
44	103.4	4.8	3414	2	US-07-373-320-3	Sequence 3, Appl1
45	101.8	4.7	1953	2	US-08-315-468-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-09-001-982-9
; Sequence 9, Application US/09001982
; Patent No. 6204246
; GENERAL INFORMATION:
; APPLICANT: Bosch, Hendrick J.
; APPLICANT: Stiekema, Willem J.
; TITLE OF INVENTION: Hybrid Toxin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6204246artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/602,737
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3468 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3468

US-09-001-982-9

Query Match 8.0%; Score 172.4; DB 3; Length 3468;
 Best Local Similarity 54.2%; Pred. No. 5,6e-32;
 Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

287 GGGATCAGTCTCGATATATAGTATGAGACATACCTTATACATTTCTGTAAC 346
 158 GCGATGACGAAAGAAAGACAGATATCTATGGGACAAACATAGCTCTTATACAGCAC 217
 347 CCGGATAGGTGGAATTCCTGTAATTTT-----CAATATATAAACAATCTATCCGT 400
 218 CTCTCTACTGATTAATTTCAATAGTATAGACCTTATAGTAAAGTCTAGAGGATA 277
 401 CTCTGCTCATCTGTCGACGACTTTCTATATGATTTAGTATCTATATTCGTAAG 460
 278 GTAGTGAACAATCAATATGATTTGCTATATGATGACTTATATCTATATTAATTTAC 337
 461 AGGTAGACGAGCGGTGTAAGTGAAGGGGTGCAATTTGAGGGTGAATGACTGCTT 520
 338 GGGTAACTGAGATGTTTAAATGATGGGATTCGAAATTTAATGTTCTGTACTTAT 397
 521 ATCAAGATTATATCTTC-----ATTATCTTGAGATTGGCTTACAGATA 565
 398 ACAGAACTATTTAGAGGCTCTGGATAGCTGAATAAGATCTTAATTCGTTCTGCTG 457
 566 AATCAATCTTAAAAAATCTGTCGACTTAAACGTTCCAGACGCGGAAGAAAT 625
 458 AAGAACTCGGTACTGTTTAAATGCGCAGCTCAGAAATTTGATGAATTTTAAACCGAG 517
 626 TCACATACTTTAGCAGGCTCATTTATCAAGACAGAAAGCTGAATTTATTTATTCCTA 685
 518 GGTCTTTAAGGATGGGCTGCTGTTAGTACAGAAATGCCCAATTTATTTATTCCTT 577
 686 CGTATGTCAGCTGCAATATGTCATTTATTTATTTAGGAGCGAGTTAAATATATATAA 745
 578 CTTTTCGAGCGCTGCAATTTTCCATTTATTTACTATAGAGGATGCTACTAGATAGGCA 637
 746 AAGAAATGGGACATAGTGTCCACCGTTATCCAGGGTCAAGGAACTGATTTGTAAG 805
 638 CTAAATGGGGGTATACAAATGCTACACCTTTTATTA-----ATTATCAAT 682
 806 AGCGTTTAAAGCGAAATATAAGAGTATCTAATTTATGAGGTGATATACAG 865
 683 CAATACTAGTAGCTTATTTGAATATATCTATATTCGTAATTTGATATATACAG 742
 866 GTTTAATCATGATTAAGACAGCGCGGTACAAATGCTGAAGTTTGTGCAATTTAATTAAT 925
 743 GTTTCAACGAATTAAGACAGAGCAAGGCACTAGTGTACAGCTTGTGTTAGATTTCAAT 802
 926 TTGCTGAGAAATGACGCTTGGCGTATTTGATATTTATTTGCTATATTTCCAACTATGAT 985
 803 ATGTGAGAGATGACATTTATGATGATTTAGTATAGTATGATCATTTTCAAGCTTGATA 862
 986 TTGAAATAATTCATTAGCAAGTGTAGATTAATAGGAAATTTATAGATCCAG 1045
 863 TTACTATATTCCTAATTAAGAAACAGATTTTCAAGTTGATGAGGATCATTTATACATCCAA 922
 1046 TGGGATATTCAGGGGGAATTAATGTTGGAA 1077
 923 TTGTTTGTGATCATGATGATGCTTTAGGGGA 954

RESULT 2

US-09-668-650-9

Sequence 9, Application US/09668650

Patent No. 6780408

GENERAL INFORMATION:

APPLICANT: Boesch, Hendrick J.

TITLE OF INVENTION: Hybrid Toxin

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSER: No. 6780408artis Corporation
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/668,650
 FILING DATE: 22-Sep-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/001,982
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/602,737
 FILING DATE: 21-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-541-8587
 TELEFAX: 919-541-8689
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3468 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Bacillus thuringiensis
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3468
 SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 US-09-668-650-9

Query Match 8.0%; Score 172.4; DB 3; Length 3468;
 Best Local Similarity 54.2%; Pred. No. 5,6e-32;
 Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

287 GGGATCAGTCTCGATATATAGTATGAGACATACCTTATACATTTCTGTAAC 346
 158 GCGATGACGAAAGAAAGACAGATATCTATGGGACAAACATAGCTCTTATACAGCAC 217
 347 CCGGATAGGTGGAATTCCTGTAATTTT-----CAATATATAAACAATCTATCCGT 400
 218 CTCTCTACTGATTAATTTCAATAGTATAGACCTTATAGTAAAGTACTAGAGGATA 277
 401 CTCTGCTCATCTGTCGACGACTTTCTATATGATTTAGTATCTATATTCGTAAG 460
 278 GTAGTGAACAATCAATATGATTTGCTATATGATGACTTATATCTATATTAATTTAC 337
 461 AGGTAGACGAGCGGTGTAAGTGAAGGGGTGCAATTTGAGGGTGAATGACTGCTT 520
 338 GGGTAACTGAGATGTTTAAATGATGGGATTCGAAATTTAATGTTCTGTACTTAT 397
 521 ATCAAGATTATATCTTC-----ATTATCTTGAGATTGGCTTACAGATA 565
 398 ACAGAACTATTTAGAGGCTCTGATAGCTGAATAAGATCTTAATTCGTTCTGCTG 457
 566 AATCAATCTTAAAAAATCTGTCGACTGATTAACAGTTCACAGACGCGGAAGAAAT 625
 458 AAGAACTCGGTACTGTTTAAATGATGCGCACTCGAATTTGATGAAATTTTAAACCGAG 517
 626 TCACATACTTTAGCAGGCTCATTTATCAAGACAGAAAGCTGAATTTATTTATTCCTA 685
 518 GGTCTTTAAGGATGGGCTGCTTATAGTACAGAAATGCCCAATATATTTATTAATCTT 577


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QY      686 CGTATGTCAGAGCTGCAAAATGTCATTTACTATTAGGAGCGAGTTAAATATAAA 745
Db      578 CTTTGGGAGGCGTGCATTGTTTCACTATTACTAGGAGGAGTCTACTAGATATGCA 637
QY      746 AAGATGGGGAGCTAGTGTGTCACCGTGTATCCAGGGGTGAGGAGAACTATGTAGC 805
Db      638 CTAATTGGGGCTTATCAATCTCTACACCTTTTATA-----ATTATCAAT 682
QY      806 AGCGGTTAAAGCCGAAATTAAGATATCTAATTTATGTAGGGTGTATAAAG 865
Db      683 CAAACTAGTAGAGCTTATTGAATATATCTGATTTGCTGATTTGATATACAG 742
QY      866 GTTATGATCAGATTAAGACAGCGGGTACAGTGTCTGAATTTGATATAAT 925
Db      743 GTTTCACGAACTAAGACAGGAGGCACTAGTGTACAGCTTGTGTAATTTCAATGAT 802
QY      926 TTGTTAGGAATAGCTGGCGGTATTTGATATTTATTTTCCACTATGAT 985
Db      803 ATCTAGAGAGATACATTGATGATATAGATAGATCAATTTTCAAGTCTTATATA 862
QY      986 TTGAAAAATATCCATTAGCAACAAGTATAGATTAACTAGGGAATTTATCAGATCCAG 1045
Db      863 TTACTATTTACCAATAGAAACAGATTTTCAAGTGTAGAGGTCATTTATCAATCCA 922
QY      1046 TGGATATTCAGGGGGAAATTATGCTTGGGAA 1077
Db      923 TTGGTTTGTACATCGTAGTAGTCTTAGGGA 954

```

RESULT 3

US-09-002-285-71
; Sequence 71, Application US/09002285
; Patent No. 6369213

GENERAL INFORMATION:

APPLICANT: Schneck, H. Ernest
APPLICANT: Micker, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Peets
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patencin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-002-285-71

Query Match 8.0%; Score 172.4; DB 3; Length 3471;
Best Local Similarity 54.2%; Pred. No. 5.6e-32;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

```

QY      287 GGGATCAGCTCGGATATAGTAATCTATGGGACATACCTTATCAATCTTGTAGAAC 346
Db      158 GCGATGCGAGAAAAGAGAGATCTATTTGGGACAAACCATAGTCTCTTATCACAGCAC 217
QY      347 CCGGTATAGGTGGAATCCGTATATTTT-----CAATATTAACAACCTACCTCCGT 400
Db      218 CTTCTCTTACTGATTAATTAATTAATAGATATAGACCTTATAGGTAAGTACTAGAGGTA 277
QY      401 CTTCTGTCATCTGTGGCAGCACTTCTATATGTAGATTAGTATCTATATTTGTAAG 460
Db      278 GTAGTGACAAATCATATCAGATTGCTATATGTACTTATATCTATTTATTTATTTAC 337
QY      461 AGTAGACGAGAGCGTGTAAAGTACGCGGGTTGCAATTTTGAAGGTAATGACTGCTT 520
Db      338 GGGTATGACAGAGTGTTTTAAATGATGGATGAGATTTTAAATGTTCTGTACTCTTAT 397
QY      521 ATCAAGTATATATCTT-----ATTATCTTGAAGATTGCTTACAGATA 565
Db      398 ACAGAACTATTTAGAGCGCTCTGTAGATCTGGAATTAAGAACTTAACTTCTGCTCTG 457
QY      566 AATCAAACTCTTAAAAAATCTGTGACGTAGTTAAACAGTTTCCAGCAAGGAGAGAAAT 625
Db      458 AAGAACTCCGTAATCTGTTTAAATGATCCGACATCAAGATTTGATAGATTTTAAACCGAG 517
QY      626 TCACTAACTTTTACGAGGTCATTTATCAAGACAGAAAGCTGAATATTTATTTGCTTA 685
Db      518 GGTCTTTAAAGAAATGAGGCTCGTTAGCTAGACAAATGCCCCAAATATTTATTTACTT 577
QY      686 CGTATGTCAGAGCTGCAAAATGTCATTTATCTATTAAGGAGCGCATTAATATAAA 745
Db      578 CTTTGGAGCGCTGCATTTTCCATTTATTTACTACTAGAGGATGATAGATATGCA 637
QY      746 AAGATGGGAGCTAGTGTGCCACCGTGTATCCAGGGGTGAGGAGAACTGATTTAGC 805
Db      638 CTAATTGGGGCTATACAAATGCTACACCTTTTATA-----ATTATCAAT 682
QY      806 AGCGGTTAAAGCCGAAATTAAGATATCTAATTTGTAGGGTGTATAAAG 865
Db      683 CAAACTAGTAGAGCTTATGAACTATATCTGATTTTCGTACATTTGATATGAG 742
QY      866 GTTATGATCAGATTAAGACAGCGGGTACAGTGTCTGAATTTGTCGAAATTTATATAAT 925
Db      743 GTTTCACGAACTAAGACAGGAGCTAGTGTCTACAGCTTGTGTAATTTCAATGAT 802
QY      926 TTGTTAGGAATAGCTGGCGGTATTTGATATTTATTTGCTATATTTTCCACTATGAT 985
Db      803 ATCTAGAGAGATGACATTATGATATTTAGATATAGATCATTTTCAAGTCTTATATA 862
QY      986 TTGAAAAATATCCATTAGCAACAAGTATAGTTAACTAGGGAATTTATCAGATCCAG 1045
Db      863 TTACTATTTACCAATAGAAACAGATTTTCAAGTGTAGAGGTCATTTATCAAGATCCA 922
QY      1046 TGGATATTCAGGGGGAAATTATGCTTGGGAA 1077
Db      923 TTGGTTTGTACATCGTAGTAGTCTTAGGGA 954

```

RESULT 4

US-09-589-477-71
; Sequence 71, Application US/09589477
; Patent No. 6570005

```

; GENERAL INFORMATION:
; APPLICANT: Schneck, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stockhoff, Brian
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/589,477
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-589-477-71

Query Match      8.0%; Score 172.4; DB 3; Length 3471;
Best Local Similarity 54.2%; Pred. No. 5.6e-32;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 287 GGAATAGTCTGGATATAGTAACTTTGGGACATACCTTATACAACTTCTGCTAGAAC 346
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 158 GCGATGACGAGAAAGAGAGATCTATGAGACACCATAGTCTCTATACACAGCAC 217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 347 CCGATATAGGATCTGATATATTTT-----CAATAATAACAACCTATTCGT 400
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 218 CTCTCTTACTGATTAATTCATATATATGACCTTAATGATTAAGTAACTAGAGAGTA 277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 401 CTCTGTCATCTGTGGACACCTTCTATATGTGATTAAGTATTAATTCATTAATTCGTAAG 460
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 278 GTAGTGCACATCATATCAGATTGTCTATATGTGACTTATATATTAATTAATTTAC 337
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 461 AGGTAGCAGAGCGGTGTTAAGTACGGGGTTCAGATTGAGGGTGAATGACGCTT 520
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 338 GGGTAAGTCAAGAGGTTTAAATGATGGATTCGAGATTTTAATGTTCTGTACTCTTAT 397
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 521 ATCAAGATTATTAATCTTC-----ATTATCTGAGAGTTGGCTTACAGATA 565
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DB 398 ACAGAACTATTAGAGGCTCTGATAGCTGGAATTAAGAACTCTTAATTTGCTTCTGCTG 457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 566 AATCAAACTCTAATAAACTTGCTGACGTAGTTAAACAGTTCCAGACGGGAAGAGATT 625
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DB 458 AAGAACTCCGTACTGTTTAGAATGCCGACCTCAAAATTTGATAGATTTTAAACCCGAG 517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 626 TCACTAACTTTTACAGAGGCTCATTTATCAAGACAGAAAGCTGAATATTTATTTGGCTTA 665
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 518 GGTCTTTAAGCATGTGTGCTGCTTATGCTAGACAAATCCCAATATTAATTAATTCCTT 577
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 686 CGTATGCAAGCTGCAAAATGTCATTTATTTCTATTAAGGAGCGAGTTAAATATATAA 745
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 578 CTTTTCGAGCGCTGATTTTTCATTTATTTACTTAAGGATGCTTACTAGATAGGCA 637
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 746 AAGATGGGACTAGTGTGTCCACCGTTGTATCCAGGTCAGGAGAACTGATTTGTAAG 805
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 638 CTAAATGGGGGCTATCAATGCTACACCTTTATAA-----ATTATCAAT 682
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 806 AGCGTTTAAAGCGGAAATTAAGAGTATCTAATTTATTTGTAGGCTGATTAACAAG 865
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 683 CAAACTAGTAGGCTTATTTGAACATTAATACGATTAATGCGTACATTTGTATTAATCGAG 742
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 866 GTTTAGATCAGATTAAGACAGCGGGGTACAGTGTGAAGTTTGTGCAATTAATAAT 925
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 743 GTTTCAACGACTATACACACGAGCACTAGTCTACAGCTTGTTAGATTTTCAATAGAT 802
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 926 TTGCTAGAGAAATGACGTTGCGGATTTGGAATTAATTTCTATATTTTCAACTTATGATT 985
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 803 ATCGTAGAGAGATGATGATGATGATTAATGATTAAGTATGATGATCATTTTCAAGCTTGATA 862
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 986 TTGAAATAATTCATTAAGCAACAGTGTAGATTAAGTGAAGAAATTTATTAAGATCCAG 1045
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 863 TTACTAATTAATCCAAATGAACAGATTTTCAGTTGATGAGGTCATTTATTAACAGATCCA 922
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1046 TGGATATTCAGGGGGAATTAATGTTGGGAA 1077
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 923 TTGCTTTGATCACTGCTAGTATGATGAGGGA 954
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
US-10-099-285A-71
; Sequence 71, Application US/10099285A
; Patent No. 6752992
; GENERAL INFORMATION:
; APPLICANT: Schneck, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stockhoff, Brian
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/099,285A
; FILING DATE: 02-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/002,285
; FILING DATE: 31-DEC-1997
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; ATTORNEY/AGENT INFORMATION:
```

NAME: Sanders, Jay M.
 REGISTRATION NUMBER: 39,355
 REFERENCE/DOCKET NUMBER: MA-701C2D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (352) 375-8100
 TELEFAX: (352) 372-5800
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3471 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 71:
 US-10-099-285A-71

Query Match .8.0%; Score 172.4; DB 3; Length 3471;
 Best Local Similarity 54.2%; Pred. No. 5.6e-32;
 Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

287 GGAATACATCTCGAATATAGTAATTAATGGAGACATTAATCAATCTTCTGTAAGC 346
 158 GCGATGACGAAAGAGACATATCTATGGGACACCATATGCTCTCTATACAGAC 217
 347 CCGGTATAGTGAATTCCTGTAATTTT-----CAATATTAACAACATCTATCCGT 400
 218 CTCTCTTACTGATTAATTAATTAATGACCTTAATAGTAAAGTCTAGAGGTA 277
 401 CTCTGTCATCTGTCGACGACCTTCTATATGATTAATTAATTAATTAATGTAAG 460
 278 GTATGACATCATATCATATTTGCTATATGATTAATTAATTAATTAATTAATTA 337
 461 AGGTAGACGAGCGGTGAATGACGCGGTGACAGATTTGAGGTAATGACCTCT 520
 338 GGGTAAGTCAGAGTGTAAATATGAGATGACATTTTAATGTTGTAATCTAT 397
 521 ATCAAGTTATATCTTC-----ATTATCTGAGGATTTGCTTACAGATA 565
 398 ACAGAACTATTAAGAGCTCTGATGACGGAATTAAGAAATCTTAATCTGCTCTG 457
 566 ATCAAAATCTTAATAAACTTGTGACGATTAACAGTTCCAGACGCGGAATTAAT 625
 458 AAGAACTCTGATCTGTTTGAATGCGGACCTAGAAATTTGATTAATTAATTA 517
 626 TCACTAACTTTTGAAGGCTATTAATCAAGACGAAAGTGAATTAATTAATTA 685
 518 GGTCTTAACGAATGGGCTGTTAGTACGACAAATGCGCAATTAATTAATTA 577
 686 CGTATGCAAGTCGAAATGTCATTTTACTTATTAAGGACGCGATTAATTAAT 745
 578 CTTTGGAGCGCTGCAATTTTCCATTTTACTTAAAGGATGCTTAAAGATGACA 637
 746 AAGAACTGCTGATGTCACCGTTGATCCAGGCTCAGGGAATTAATTAATTA 805
 638 CTAAATGGGGCTTAAATGCTACACCTTTTAA-----ATTATCAAT 682
 806 AGCGTTAAAGCGAAATTAAGATTAATTAATTAATTAATTAATTAATTAAT 865
 683 CAAACTAGTAGCTTATGAATTAATTAATTAATTAATTAATTAATTAATTA 742
 866 GTTTAGTCAATGACGAGCGGTGACAGTCTGAAAGTTGCTGAAATTAATTA 925
 743 GTTTCACGAACTAAGACGAGGCTGATGCTTAAAGCTGTTGAAATTAATTA 802
 926 TTCTGATGAATGACGTTGGCGGTATTTGATTAATTAATTAATTAATTAATTA 985
 803 ATGCTAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 862
 986 TTGAAAAATATCCATTAGCAACAGTGAATTAATTAATTAATTAATTAATTA 1045
 863 TTCTAATTAATCCCAATTAAGAAAGATTTTCAAGTGAAGGCTATTAATTA 922
 1046 TGGATATTTGAGGCGGAAATTAATTAATTAATTAATTAATTAATTAATTA 1077

Db 923 TTGGTTTGTATCATCTAGTATGCTTAAAGGGA 954

RESULT 6
 US-09-001-982-11
 Sequence 11, Application US/09001982

Patent No. 6204246
 GENERAL INFORMATION:
 APPLICANT: Bosch, Hendrick J.
 APPLICANT: Stiekema, Willem J.
 TITLE OF INVENTION: Hybrid Toxin
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESSES:
 ADDRESSER: No. 6204246artis Corporation
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/001,982

FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/602,737

FILING DATE: 21-FEB-1996
 ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8587
 TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:

LENGTH: 3726 base pairs
 TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: cDNA
 FEATURE:

NAME/KEY: CDS
 LOCATION: 1..3726

US-09-001-982-11

Query Match .8.0%; Score 172.4; DB 3; Length 3726;
 Best Local Similarity 54.2%; Pred. No. 5.7e-32;
 Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

287 GGAATACATCTCGAATATAGTAATTAATGGAGACATTAATCAATCTTCTGTAAGC 346
 158 GCGATGACGAAAGAGACATATCTATGGGACACCATATGCTCTCTATACAGAC 217
 347 CCGGTATAGTGAATTCCTGTAATTTT-----CAATATTAACAACATCTATCCGT 400
 218 CTCTCTTACTGATTAATTAATTAATTAATGACCTTAATAGGTAATTAATTAATTA 277
 401 CTCTGTCATCTGTCGACGACCTTCTATATGATTAATTAATTAATTAATGTAAG 460
 278 GTATGACATCATATCATATTTGCTATATGATTAATTAATTAATTAATTAATTA 337
 461 AGGTAGACGAGCGGTGAATGACGCGGTGACAGATTTGAGGTAATGACCTCT 520
 338 GGGTAAGTCAGAGTGTAAATATGAGATGACATTTTAATGTTGTAATCTAT 397
 521 ATCAAGTTATATCTTC-----ATTATCTGAGGATTTGCTTACAGATA 565

Db 398 ACAGAACTATTGAGGCTCTGAGATAGCTGAATGAATCTTAATTCCTTCCTGCTG 457
QY 566 AATCAATCCTAATAAACTTGTGAGTAGTATAACAGTCCAGACGGGAGAGATT 625
Db 458 AAGAACTCGTACTCGTTTGAATCGCCACTCAGAAATTGATGAAATTTTAAACCCGAG 517
QY 626 TCACATACTTTTGAAGAGGCTCATTTACAGACAGAAAGCTGAATATTTATTTGCTTA 685
Db 518 GGTCTTTAAGAAATGGGCTCGTTAGCTAGACAAATATGCCAAATTTATTTATTCCTT 577
QY 686 CGATGTGCAAGCTGCAGATGTGCATTTATTTACTATTAGGAGCGCATTAATATPAAA 745
Db 578 CTTTTCGAGCGCTGATTTTTCATTATTACTAGAGGATGCTACTAGATGATGCGCA 637
QY 746 AAGATGGGAGCTAGTGTGTCCACCGTTGATCCAGGGTCAGGAGAACGATTTGATAG 805
Db 638 CTAAATGGGGCTATATCAATGCTACACCTTTTATA-----ATTATCAAT 682
QY 806 AGCGGTTAAAGCGAAATTAAGATATCTAATTATGTGTAGGGTGTATPACAGG 865
Db 683 CAAACTAGTAGAGCTTATGAACTATATCTGATTATGCGTACATTTGGTATATTCGAG 742
QY 866 GTTTAATCAGATTAAGACAGCGCGGTACAGTGTGCAAGTTTGGTGAATTTAATPAA 925
Db 743 GTTTCACGAACTAAGCAACAGGCACTAGTGTCTACGCTTGTAGAAATTTTCATAGAT 802
QY 926 TTGCTAGAGAAATGACGTTGGCGGTATTTGATATTTATGCTATATTTTCCAACTTATGAT 985
Db 803 ATCTAGAGAGATGACATTATGTATTTAGATATAGTAGCATCATTTTCAAGCTTGATA 862
QY 986 TTGAAAAATATTCATTAGCAACAAGGTGTAGATTAAGTGAATTTATPACAGATCCAG 1045
Db 863 TTACTATATTCACCAATGAAACAGATTTTCAGTTGATAGGATTCATTATPACAGATCCA 922
QY 1046 TGGGATATTTCAGGGGGAATTAATGTTGGGAA 1077
Db 923 TTGGTTTGTACATCTGATAGTCTTAGGGGA 954

RESULT 7
US-09-668-650-11
Sequence 11, Application US/09668650
Patent No. 6780408
GENERAL INFORMATION:
APPLICANT: Bosch, Hendrick J.
TITLE OF INVENTION: Hybrid Toxin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 6780408artis Corporation
STREET: 3054 Cornwalis Road
City: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/668,650
FILING DATE: 22-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/001,982
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/602,737
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP

TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3726
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-668-650-11

Query Match 8.0%; Score 172.4; DB 3; Length 3726;
Best Local Similarity 54.2%; Pred. No. 5.7e-32;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 287 GGGATTCAGTCCGGATATAGTAACTTTGGGACATACCTTATACAAATCTTGTAAGC 346
Db 158 GCGATGCAACAAAGAGCAGTATCTATTGGACAACTAGTCTCTCTTATCAGACAC 217
QY 347 CCGGATAGGTGAATTCCTGTATATTTT-----CAATATPAAAACAACCTCATTCCT 400
Db 218 CTTCTCTTATCTGATTAATTTCAATAGTATATGACCTTATATAGTAAGTACGAGATA 277
QY 401 CTTCTGTCAATCTGTGACGACCTTTATATGTGATTTAGTATCTATTAATTCGTAAG 460
Db 278 GTAGTGAACAACTCATCATCAGATTTGTCTATATGTGACTTATATCTATTAATGATTTAC 337
QY 461 AGGTAGACAGACCGGTAAAGTGAAGACGGGCTGACATTTTGAAGGTGAATGACGCTGT 520
Db 338 GGTATAGTCAGAGTGTATTAATTAAGATGAGATTCAGATTTTAATGCTGTACTCTTAT 397
QY 521 ATCAAGATTAATTAATTC-----ATTATCTGAGATTTGGCTTACAGATA 565
Db 398 ACAGAACTATTTAGAGGCTCTGATAGCTGAATPAAATCTTAATCTGCTTCGCTG 457
QY 566 AATCAATCTTAAAACTTGTGACGTAGTTAAACAGTTCCAGACGGGAGAAAGATT 625
Db 458 AAGAACTCGTACTCGTTTGAATCGCCAGCTCAGAAATTTGATGAAATTTTAAACCCGAG 517
QY 626 TCACATACTTTTGAAGAGGCTATATCAAGACAGAAAGCTGAATATTTATTTGCTTA 685
Db 518 GGTCTTTAAGAAATGGGCTGTGATGCTAGACAAATATGCCAAATATTTATTTACCTT 577
QY 686 CGATGTGCAAGCTGCAGATGTGCATTTATTTACTATTTAAGGAGCGCATTAATATPAAA 745
Db 578 CTTTTCGAGCGCTGATTTTTCATTATTTACTAAGGATGCTACTAGATATGCGCA 637
QY 746 AAGATGGGAGCTAGTGTGTCCACCGTTGTATCCAGGGTCAGGAGAACTGATTTGATAG 805
Db 638 CTAAATGGGGCTATATCAATGCTACACCTTTTATA-----ATTATCAAT 682
QY 806 AGCGGTTAAAGCGAAATTAAGATATCTAATTATTTGTTAGGGTGTATPACAGG 865
Db 683 CAAACTAGTAGAGCTTATTTGAATCTATATAGATTTATGCGTATATGATTAATTCGAG 742
QY 866 GTTTAATCAGATTAAGACAGCGCGGTACAGTGTGCAAGTTTGGTGAATTTAATPAA 925
Db 743 GTTTCACGAACTAAGACAGAGGCACTAGTGTCTACAGCTTGTGTAATTTCAATAGAT 802
QY 926 TTGCTAGAGAAATGACGTTGGCGGTATTTGATATTTATTTGCTAATTTTCAACTTATGAT 985
Db 803 ATCTAGAGAGATGACATTTGATGTATGATATAGTATGATGATCAATTTTCAAGCTTGATA 862
QY 986 TTGAAAAATATTCATTAGCAACAAGGTGTAGATTTAAGTGAATTTTAAAGATCCAG 1045
Db 863 TTACTATATTCACCAATGAAACAGATTTTCAGTTGATGAGGTGATTTATPACAGATCCA 922
QY 1046 TGGGATATTTCAGGGGGAATTAATGTTGGGAA 1077

GENERAL INFO ;

APPLICANT: Donovan, William P.
APPLICANT: Tan, Yeping
APPLICANT: Jany, Christine S. M.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,046
FILING DATE: 06-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egoif, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3934 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 67..3756
FEATURE:
NAME/KEY: misc feature
LOCATION: 2253..2272
US-08-779-046-3

Query Match 5.5%; Score 118.2; DB 2; Length 3934;
Best Local Similarity 54.8%; Pred. No. 8.4e-19;
Matches 293; Conservative 0; Mismatches 218; Indels 24; Gaps 2;

QY 561 AGATTAATCAATCTTAAAAAAGTCTGACGTAATTAAACAGTTCCAGACAGGGAAGA 620
DB 492 AGATTAACCGAAATGACAGATCAAGAACATTATCTTGACGCTATGCTTTAGA 551
QY 621 AGATTTCACCTAACTTTTACAGAGGTATATATCAAGACAGAAAGCTGAATATATTTT 680
DB 552 ACTTGACATTACTACTGCTATACCGCTTTTCAGAAATGAGAAAGAAAGTTCCATTATT 611
QY 681 GCCTAGTATGTCAGAGTCAATATGTCATTTATTTATTTAAGGACGACAGTAAATA 740
DB 612 AATGATATATGCTCAAGCTGCAATTTACACCTATTTATTTAGAGAGCCATCCCTTTT 671
QY 741 TAAAAAAGAAATGGGACTAGTGTGTCACCGTTGTATCCAGGGTCAAGGAGAACTGATTG 800
DB 672 TGTAGTGAATGGGGATGCGATCTTCGATGTTAACCA-----TA 713
QY 801 TAAAGAGCGGTAAAGCGAAATTAAGAGTATACATTAATTTAGTACGCTGATATA 860
DB 714 TTACCAAGAAACAATATGATATATCAAGGAGATATTTTACCAATTTGCTACAAATGATATA 773
QY 861 CAAGGTTTATGATCAGATTAAGACAGCGGGTACAGTGTGAAGTTTGTGCAAAATTTAA 920

DB 774 TACAGGCTAAATTACTTAAG-----CGGCAATGCTGAAGTTGGTCGGTATTA 827
QY 921 TAAATTTGAGAGAAATGACCTTGCGGTATTTGATTAATTTGCTAATTTCCAACTTA 980
DB 828 TCAATTCCTGAGACCTTAAGGAGTATTAAGTATTAAGAGCCCTATTCGCAAGCTA 887
QY 981 TGAATTTGAAAAATTCCTTATGCAACAGTGTAGAGTAACTAGGAAATTTATACGA 1040
DB 888 TGAATCTGCACTTATTCATATACAGTGTCTGATTAACAGAAATTTATACAGA 947
QY 1041 TCCAGTGGATATTAAGGGGAAATTAAGTTGGAAACGTTTATTTAGCTTAAT 1095
DB 948 TCCATTTGGAGAAACAATGACCTTCAGAGTTTGCAAGTATGATTTAT 1002

RESULT 14
US-08-881-340-3
Sequence 3, Application US/08881340
Patent No. 5942658
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yeping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,340
FILING DATE: 24-JUN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egoif, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3934 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 67..3756
FEATURE:
NAME/KEY: misc feature
LOCATION: 2253..2272
US-08-881-340-3

Query Match 5.5%; Score 118.2; DB 2; Length 3934;
Best Local Similarity 54.8%; Pred. No. 8.4e-19;
Matches 293; Conservative 0; Mismatches 218; Indels 24; Gaps 2;

QY 561 AGATAAATCAATCTTAAATAAAGTGTGAGTAGTAAAGTTCACAGACGGGAGA 620
 DB 492 AGATACCGAATATGATGCAATCAAGAGCATATTTCTGAGCGCTATGTCTTAGA 551
 QY 621 AGATTCACTAACTTTAGCAGGGCTCATTTCAAGACAGAACTGAAATATTATT 680
 DB 552 ACTGACATTTCTACTGTATACCGCTTTTCAAGAAATGAAATGAAAGTTCATTAT 611
 QY 681 GCTACGATGTGCAAGCTGCAAAATGTGCAATTTATTTAAAGGACGCAATTAATA 740
 DB 612 AATGATATGCTCAAGCTGCAAAATTTACACTATTTATTTAGAGACGATCCCTTT 671
 QY 741 TAAATAAGATGGGACACTAGTGTGCAACCGTGTATCCAGGGTCAGGAACTGATG 800
 DB 672 TGGTAGTATGGGAGTGGGATGCGATCTTCGATGTAAACCA-----TA 713
 QY 801 TAAAGACCGTTTAAAGGCAAAATTAAGATTAATTTATTTGTGAGGGTGTATA 860
 DB 714 TTACCAAGAACAAATCAGATTTACAGAGAAATTTTACCATTTGCGTACATGTATA 773
 QY 861 CAAGGTTTATGATCAGATTAAGACAGCGGGTACAGTGTGAACTTTGCTGAAATTTAA 920
 DB 774 TACAGGCTAAATTAATTAAGA-----GGGACAAATGCTGAAGTTGGTTGCGTATA 827
 QY 921 TAAATTCGTAGAAATAGAGTGTGCGGTATTTGATATTTTCTATATTTTCACTTA 980
 DB 828 TCAATTCGTAGAACCTTAACGTTTGGGATTTGATTTAGTACCCCTATTTCCAACTA 887
 QY 981 TGATTTTGAATAATATCATTAAGCAAGTGTAGATTAAGTAACTGAGGAAATTTATACA 1040
 DB 888 TGATACCTGCACTTATTCATTAAGAGTGTCACTGATTAAGAAATTTTATACAGA 947
 QY 1041 TCCAGTGGATTTTACAGGGGAAATTTATGTTGGAAACGTTTATGCTTTAAT 1095
 DB 948 TCCATTTGGAGAACAAATGCACTTCAGATTTGCAAGTACGAATGTTTAAT 1002

RESULT 15
 US-08-448-170-7
 ; Sequence 7, Application US/08448170
 ; Patent No. 5723758
 ; GENERAL INFORMATION:
 ; APPLICANT: Payne, Jewel
 ; APPLICANT: Cummings, David A.
 ; APPLICANT: Cannon, Raymond J.C.
 ; APPLICANT: Narva, Kenneth E.
 ; APPLICANT: Steiman, Steve
 ; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
 ; TITLE OF INVENTION: B.t. PS158C, Active Against Lepidopteran Pests, and Genes
 ; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David R. Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: Florida
 ; COUNTRY: USA
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/448,170
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/069,902
 ; FILING DATE: 01-JUNE-1993
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/759,247

FILING DATE: 13-SEPT-1991
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: M/S 102D.C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (904) 375-8100
 TELEFAX: (904) 372-5800
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3684 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-448-170-7

Query Match 5.4%; Score 116.8; DB 2; Length 3684;
 Best Local Similarity 55.0%; Pred. No. 1.8e-18;
 Matches 310; Conservative 0; Mismatches 227; Indels 27; Gaps 3;

QY 532 TATCTTATTTATGTTGAGATGAGTGTGCTTACAGATTAATCAATCTTAAATACTGCTGAC 591
 DB 400 TATCAACAGTCACTTGAAGATGGCTAGAAAACCGTATGATGCAAGACGAGAGTGT 459
 QY 592 GTAGTTAAAGATTTCCAGACGAGGAAAGATTTCACTAACTTTAGCAGGGTCAATTA 651
 DB 460 CTTATATCCAAATATATAGCTTAGAAGCTTATTTCTTATATGATGCGCTTTGGCA 519
 QY 652 TCAAGACAGAAAGCTGAAATTTATTTATGCTTACATGATGCAAGCTGCAATGTGCAT 711
 DB 520 ATTGAACCAAGAAAGTCCATTTATATG---GTATATGCTCAAGCTGCAAAATTTACAC 576
 QY 712 TTAATTTCTATTAAGGAGCGAGTAAATATTAATAAATGCGGACATGCTGCCACCG 771
 DB 577 CTATATTTATTTAGAGATGCTCTCTTTTGTATGTAATTTGGCTTAATCCCAAGAA 636
 QY 772 TTGATTCAGAGGCTCAGGAGAACTGATTTGTAACGAGCGTTAAAGCGGAAATTAAGAG 831
 DB 637 ATTCAACG-----TTATTTAGAGCGCAAGTGGAAAAACGAGAGAA 678
 QY 832 TATACATATTTATTTGTAGGCTGTATTAACAAGGTTTATGATCAATTAAGACAGCGGCT 891
 DB 679 TATTCGATTTATTTGCGCAAGATGTATTAACGCGTTTAAATATTTGAGA-----GGG 732
 QY 892 ACAAGCTGCAAGTTTGTGTGGAATTTAATAATTTCTGTGAGAAATGACGTTGGCGGTA 951
 DB 733 ACAAAATGCTGAAAGTGTGTGCGATTAATCAATTCGTAGAGACTTAACGCTAGAGATA 792
 QY 952 TTGATATTTATTTCTATATTTTCAACTTATGATTTTGAATAAATTCATTAAGCAACAGT 1011
 DB 793 TTGATCTATGCTGACATTTCCAGAGTATGACACCGGTGTTTATCCAAATATACAGT 852
 QY 1012 GTAGAGTTAACTAGGAAATTTATTAACAGATTCAGTGGGATTTTCAAGGAGAAATTTATGT 1071
 DB 853 GCTCAATTAACAAGAAATTTATTAACAGATTCATTTGAGAGAAACCAATGACCTTCAGGA 912
 QY 1072 TGGGAACGTTTTTTAGCTTTAAT 1095
 DB 913 TTTGCAAGTACGAATGTTTAAT 936

Search completed: December 19, 2005, 13:03:16
 Job time : 273.352 secs

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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:54:29 ; Search time 200.901 Seconds
(without alignments)
5233.604 Million cell updates/sec

Title: US-10-782-141-1

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA_New:*

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9: /cgn2_6/ptcodata/1/pubpna/US11_NEW_PUB_seq:.*
10: /cgn2_6/ptcodata/1/pubpna/US60_NEW_PUB_seq:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	4.9	1860	US-11-058-727-15	Sequence 15, Appl
2	105	4.9	1860	US-11-108-389-15	Sequence 15, Appl
3	105	4.9	2010	US-11-058-727-11	Sequence 11, Appl
4	105	4.9	2010	US-11-108-389-11	Sequence 11, Appl
5	105	4.9	3621	US-11-058-727-1	Sequence 1, Appl
6	105	4.9	3621	US-11-108-389-1	Sequence 1, Appl
7	105	4.9	4874	US-11-058-727-17	Sequence 17, Appl
8	105	4.9	4874	US-11-108-389-17	Sequence 17, Appl
9	101.8	4.7	2019	US-11-058-727-55	Sequence 55, Appl
10	101.8	4.7	2019	US-11-058-727-87	Sequence 87, Appl
11	101.8	4.7	2019	US-11-108-389-55	Sequence 55, Appl
12	101.8	4.7	2019	US-11-108-389-87	Sequence 87, Appl
13	100.2	4.7	2019	US-11-058-727-59	Sequence 59, Appl
14	100.2	4.7	2019	US-11-058-727-91	Sequence 91, Appl
15	100.2	4.7	2019	US-11-108-389-59	Sequence 59, Appl
16	100.2	4.7	2019	US-11-108-389-91	Sequence 91, Appl
17	99.4	4.6	4359	US-11-091-643-3	Sequence 3, Appl
18	98.6	4.6	1863	US-11-058-727-19	Sequence 19, Appl
19	98.6	4.6	1863	US-11-108-389-19	Sequence 19, Appl
20	98.6	4.6	2019	US-11-058-727-57	Sequence 57, Appl
21	98.6	4.6	2019	US-11-058-727-89	Sequence 89, Appl
22	98.6	4.6	2019	US-11-108-389-57	Sequence 57, Appl
23	98.6	4.6	2019	US-11-108-389-89	Sequence 89, Appl

24	98.6	4.6	2022	7	US-11-058-727-7	Sequence 7, Appl
25	98.6	4.6	2022	7	US-11-058-727-21	Sequence 21, Appl
26	98.6	4.6	2022	7	US-11-058-727-25	Sequence 25, Appl
27	98.6	4.6	2022	7	US-11-058-727-29	Sequence 29, Appl
28	98.6	4.6	2022	7	US-11-058-727-33	Sequence 33, Appl
29	98.6	4.6	2022	7	US-11-058-727-43	Sequence 43, Appl
30	98.6	4.6	2022	7	US-11-058-727-49	Sequence 49, Appl
31	98.6	4.6	2022	7	US-11-058-727-67	Sequence 67, Appl
32	98.6	4.6	2022	7	US-11-058-727-69	Sequence 69, Appl
33	98.6	4.6	2022	7	US-11-058-727-75	Sequence 75, Appl
34	98.6	4.6	2022	7	US-11-058-727-81	Sequence 81, Appl
35	98.6	4.6	2022	7	US-11-108-389-7	Sequence 7, Appl
36	98.6	4.6	2022	7	US-11-108-389-21	Sequence 21, Appl
37	98.6	4.6	2022	7	US-11-108-389-25	Sequence 25, Appl
38	98.6	4.6	2022	7	US-11-108-389-29	Sequence 29, Appl
39	98.6	4.6	2022	7	US-11-108-389-33	Sequence 33, Appl
40	98.6	4.6	2022	7	US-11-108-389-43	Sequence 43, Appl
41	98.6	4.6	2022	7	US-11-108-389-49	Sequence 49, Appl
42	98.6	4.6	2022	7	US-11-108-389-67	Sequence 67, Appl
43	98.6	4.6	2022	7	US-11-108-389-69	Sequence 69, Appl
44	98.6	4.6	2022	7	US-11-108-389-75	Sequence 75, Appl
45	98.6	4.6	2022	7	US-11-108-389-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-11-058-727-15
Sequence 15, Application US/11058727
Publication No. US20050261483A1

GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flanagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnall
APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OR INVENTION: Activity
FILE REFERENCE: 35718/287809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PASCSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 1860
TYPE: DNA
ORGANISM: Bacillus thuringiensis (truncated)
FEATURE:
NAME/KEY: CDS
LOCATION: (10)...(1860)
FEATURE:
NAME/KEY: misc feature
LOCATION: (0)...(0)
OTHER INFORMATION: 49PVD
US-11-058-727-15

Query Match 4.3%; Score 105; DB 7; Length 1860;
Best Local Similarity 53.1%; Pred. No. 1.4e-15;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;
421 GCACCTTCATATGATGATTTAGATCATCTATATTCGTTAAAGGTAGACGAGCGCTTTA 480

```

Db      205 GAAATTTTATGAAACAGTAGAAGAACTCATTAATCAAAAATATAGAGATATGCAAG 264
Qy      481 AGTACGGGGTTCAGATTTTTCAGGGTGAATGACCTCTATCAAGTTATTTCTTCAT 540
Db      265 AATTAAGCGCTTCGGAATAGAGAGATAGTAAATTAACAA--TTATATCTTAAT 321
Qy      541 TATCTTGAGATTTGGCTTACAGATTAATCAATCTTAAATACTTGTGTCAGTATTA 600
Db      322 GCGCTTGAAAGATGGGAGAGAAATCCAAATGTTCAAGACCTTACAGAGATGCGCAAT 381
Qy      601 CAGTTCCAGACGCGGAGAGAAATTCATTAACCTTTAGCAGGGCTATTAACAACAG 660
Db      382 CGATTTGAAATCTGTGATAGTTATTTACCAATATATGCCA--TCCTTTAGAGTGACA 438
Qy      661 AAAGCTGAATATATATATGCTACGTATGTCAGACCTGCAATGTCATTTACTTA 720
Db      439 AATTTTGAAGTACCATTCCTTACGTATATGCAATGACCCAACTTCACTTACTGTTA 498
Qy      721 TTAAGGACCGCAGTTAAATTAATAAATAAAGGAGCTAGTGTGCCACCGTTGTATCCA 780
Db      499 TTAAGGACCGCAGTTAAATTTTGGAGAAATGGGA-----TGGTCA 540
Qy      781 GGGTCAGGAGAACTGATTTGTAACGACCGGTTAAAGCGAAATTAAGATTAAT 840
Db      541 ACAACTACTTATTAATCTATTTATGATCGTCAATGAACTTACTGCAAGATATCTGAT 600
Qy      841 TATGTGTAGGGTGTATTAACAAGGGTTTAGATCAGATTAAGACAGCGGGTATCAAGTCT 900
Db      601 CACTGTGTAAAGTGTATGAACTGCTTTCGATAGAGAAATGACACTGGCGTTTAAAGTGT 654
Qy      901 GAAGTGTGTCGAAATTTAAATTTTCGTAGAGAAATGACGTTGGCGGTATTTGATAT 960
Db      655 AAACAATGGGTGACGTATTAACAATTCGATAGAGAAATGACACTGGCGTTTAAAGTGT 714
Qy      961 ATTGCTATATTTCCAACTTATGATTTGAAAAATATCCATTAGCAACAAGTGAAGTTA 1020
Db      715 GTTGCAATTTATCCCAATTTATGACACAGCACGATCCCAATGGAAGCAACAATA 774
Qy      1021 ACTAGGGAATTTATACAGATCCAGTGGG 1049
Db      775 ACAAGGGAATTTATACAGATCCACTGGG 803

RESULT 2
; Sequence 15, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1860
; TYPE: DNA
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```

; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)...(1860)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 49PVD
US-11-108-389-15

Query Match      4.9%; Score 105; DB 7; Length 1860;
Best Local Similarity 53.1%; Pred. No. 1.4e-15;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

Qy      421 GCACCTTCTATATGATTTAGATCTATTAATTCGTAAAGAGTGAAGAGCGGTGTA 480
Db      205 GAAATTTTATGAAACAGTAGAAGAACTCATTAATCAAAAATATAGAGATATGCAAG 264
Qy      481 AGTACGGGGTTCAGATTTTTCAGGGTGAATGACCTCTATCAAGTTATTTCTTCAT 540
Db      265 AATTAAGCGCTTCGGAATAGAGAGATAGTAAATTAACAA--TTATATCTTAAT 321
Qy      541 TATCTTGAGATTTGGCTTACAGATTAATCAATCTTAAATACTTGTGTCAGTATTA 600
Db      322 GCGCTTGAAAGATGGGAGAGAAATCCAAATGTTCAAGACCTTACAGATGCGCAAT 381
Qy      601 CAGTTCCAGACGCGGAGAGAAATTCATTAACCTTTAGCAGGGCTATTAACAACAG 660
Db      382 CGATTTGAAATCTGTGATAGTTATTTACCAATATATGCCA--TCCTTTAGAGTGACA 438
Qy      661 AAAGCTGAATATATATATGCTACGTATGTCAGACCTGCAATGTCATTTACTTA 720
Db      439 AATTTTGAAGTACCATTCCTTACGTATATGCAATGACCCAACTTCACTTACTGTTA 498
Qy      721 TTAAGGACCGCAGTTAAATTAATAAATAAAGGAGCTAGTGTGCCACCGTTGTATCCA 780
Db      499 TTAAGGACCGCAGTTAAATTTTGGAGAAATGGGA-----TGGTCA 540
Qy      781 GGGTCAGGAGAACTGATTTGTAACGACCGGTTAAAGCGAAATTAAGATTAAT 840
Db      541 ACAACTACTTATTAATCTATTTATGATCGTCAATGAACTTACTGCAAGATATCTGAT 600
Qy      841 TATGTGTAGGGTGTATTAACAAGGGTTTAGATCAGATTAAGACAGCGGGTATCAAGTCT 900
Db      601 CACTGTGTAAAGTGTATGAACTGCTTTCGATAGAGAAATGACACTGGCGTTTAAAGTGT 654
Qy      901 GAAGTGTGTCGAAATTTAAATTTTCGTAGAGAAATGACGTTGGCGGTATTTGATAT 960
Db      655 AAACAATGGGTGACGTATTAACAATTCGATAGAGAAATGACACTGGCGGTTAAAGTGT 714
Qy      961 ATTGCTATATTTCCAACTTATGATTTGAAAAATATCCATTAGCAACAAGTGAAGTTA 1020
Db      715 GTTGCAATTTATCCCAATTTATGACACAGCACGATCCCAATGGAAGCAACAATA 774
Qy      1021 ACTAGGGAATTTATACAGATCCAGTGGG 1049
Db      775 ACAAGGGAATTTATACAGATCCACTGGG 803

RESULT 3
US-11-058-727-11
; Sequence 11, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
```

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/287809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 2010
TYPE: DNA
ORGANISM: *Bacillus thuringiensis* (truncated)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2010)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: 1218-1A
US-11-058-727-11

Query Match 4.9%; Score 105; DB 7; Length 2010;
Best Local Similarity 53.1%; Pred. No. 1.5e-15;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

QY 421 GCACTTCTATATGATTTAGTATCTATATCTGTTAAAGGAGGAGGAGGCTTGA 480
DB 337 GAATTTTATGGAACAGTGAAGAACTCATTAATAAAAAATGAGAAATGCAAG 396
QY 481 AGTACGGGGTTCAGATTTTGGAGGTGAATGACTGCTTATCAAGTTTATCTTCAT 540
DB 397 AATTAAGCGCTTCGGAATTAAGAGATTAAGTATATTAATCAAA--TTATATCTACT 453
QY 541 TATCTTGAGATTTGGCTTACAGATTAATCAATCTTAAAAAATTGCTGACGTATTA 600
DB 454 GCGCTTGAAAGATGGGAAGAAATCCAAATGCTTCAAGAGCTTACAGAGATGCGCAAT 513
QY 601 CAGTTCCAGCAGGGAAGAGATTTCACTTAATCTTTAGCAGGCTATTATCAAGAC 660
DB 514 CGATTTGAAATCTCGATAGTATTATTAACCAATATATGCA--TCCTTTAGAGTGACA 570
QY 661 AAAGCTGAATATATATATGCTACGATAGTGAACCTGCAATGCAATTTATTACTA 720
DB 571 AATTTTGAAGTACATTCCTTACTGTATATGCAATGCAAGCACACTTCAATTAAGTTTA 630
QY 721 TTAAGGAGCGCACTTAATATTAATAAAGAAATGGGGAAGTATGTCACCGTTGTATCA 780
DB 631 TTAAGGAGCGCGTCAATTTTGGAGAAAGATGGGGA-----TGGTCA 672
QY 781 GGGTCAGGAGAACTGATTTGTAACAGCGGTTAAAGCCGAAATAAAGAGTATTAAT 840
DB 673 ACAACTACTATTAATTAATTAATTAATGATGCTCAATGAACTTACTGCAAGATTAATTCGAT 732
QY 841 TATTTGTAGGGTGTATTAACAAGGTTTATGATGATTAAGACAGGCGGTATCAAGGCT 900
DB 733 CACTGTTAAAGTGTATGAAATCTGTTTAGCAAAATTAATA-----GGCAGAGGCT 786
QY 901 GAAAGTTGTCGAATTTAAATTAATTTGTAAGAAATGACGTTGGCGGTATTTGATAT 960
DB 787 AAACAATAGGTTGACTATTAACCAATTCGTATAGAAATGACACTGGCGGTTTATGATGTT 846
QY 961 AATGCTATTTTCCAACTTATGATTTTGAAGAAATATCACTTATGACAAAGTATGATTA 1020
DB 847 GTTGCAATTAATTCGCAAAATTAATGACACGCGTACCAATGAAAGAAAGCAACTA 906
QY 1021 ACTAGGAAATTTATACAGATCCAGTGGG 1049
DB 907 ACAAGGGAATATATACAGATCCAGTGGG 935

RESULT 4
US-11-108-389-11
Sequence 11, Application US/11108389
Publication No. US20050261188A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnall
APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/291049
CURRENT APPLICATION NUMBER: US/11/108,389
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 2010
TYPE: DNA
ORGANISM: *Bacillus thuringiensis* (truncated)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2010)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: 1218-1A
US-11-108-389-11

Query Match 4.9%; Score 105; DB 7; Length 2010;
Best Local Similarity 53.1%; Pred. No. 1.5e-15;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

QY 421 GCACTTCTATATGATTTAGTATCTATATCTGTTAAAGGAGGAGGAGGCTTGA 480
DB 337 GAATTTTATGGAACAGTGAAGAACTCATTAATCAAAATTAAGAGATTAAGGAG 396
QY 481 AGTACGGGGTTCAGATTTTGGAGGTGAATGACTGCTTATCAAGTTTATCTTCAT 540
DB 397 AATTAAGCGCTTCGGAATTAAGAGATTAAGTATATTAATTAATCAAA--TTATATCTACT 453
QY 541 TATCTTGAGATTTGGCTTACAGATTAATCAATCTTAAAAAATTGCTGACGTATTA 600
DB 454 GCGCTTGAAAGATGGGAAGAAATCCAAATGCTTCAAGAGCTTACAGAGATGCGCAAT 513
QY 601 CAGTTCCAGCAGGGAAGAGATTTCACTTAATCTTTAGCAGGCTATTATCAAGAC 660
DB 514 CGATTTGAAATCTCGATAGTATTATTAACCAATATATGCA--TCCTTTAGAGTGACA 570
QY 661 AAAGCTGAATATATATATGCTACGATAGTGAACCTGCAATGCAATTTATTACTA 720
DB 571 AATTTTGAAGTACATTCCTTACTGTATATGCAATGCAAGCACACTTCAATTAAGTTTA 630
QY 721 TTAAGGAGCGCACTTAATATTAATAAAGAAATGGGGAAGTATGTCACCGTTGTATCA 780
DB 631 TTAAGGAGCGCGTCAATTTTGGAGAAAGATGGGGA-----TGGTCA 672
QY 781 GGGTCAGGAGAACTGATTTGTAACAGCGGTTAAAGCCGAAATAAAGAGTATTAAT 840
DB 673 ACAACTACTATTAATTAATTAATTAATGATGCTCAATGAACTTACTGCAAGATTAATTCGAT 732

Qy	601	CAGTTCACAGCAGCGGGAAGAAAGATTTCACATACTTTTACAGGGTCATTATCAACAG	660
Db	514	CGATTGTGAATCTCTGGAATGTTTATTATACGCAATATATGCA---TCTTTTAGAGTACA	570
Qy	661	AAAGCTGAATATATATATATTCCTTACGATATGTCAGACTGCAATGCAATTATTA	720
Db	571	AATTTTGAAGTACCAATTCCTTACTGTATATGCAATGCAACCACTTCAATTACTGTTA	630
Qy	721	TTAAGGACGCGATTAAATATPAAAAAAGATGSGGACTAGTGTGTCCACCGTTGATCCA	780
Db	631	TTTAAAGACGCGCTCAATTTTGTGAGAAAGATGSGGGA-----TGGTCA	672
Qy	781	GGGTACGGGAGAACGATTGTATACGAGGCGTTAAACGAAATTAAGAGTACTAAT	840
Db	673	ACAACTACTATTATATACATTATATGATGTCAAATGAACTTACTGCAATATTTTGAT	732
Qy	841	TATTTGTATGGGTGTATATACAGGGTTTATGATCAGATPAAAGACGGCGGTACAGTGTCT	900
Db	733	CACGTGTATTAAGTGTATGAAGAACTGGTTTATACAAATTAATAA-----GGCAAGAGCGCT	786
Qy	901	GAAGTTTGGTCCAAATTTAATAAATTTTCGTAGAGAAATGACGTTGGCGGTATTGATATT	960
Db	787	AAACAATGGGTGTACATATPAAACAATTCGTATGAAATAATGACACTGGGCGTTTATGATGTT	846
Qy	961	ATTGTATATTTTCCAACTTATGATTTTGAAAAAATATCATTAGCAACAGTATAGATTA	102
Db	847	GTTTGCATTATTTCCCAATTTATGACACACGACGTCATCCCAATGAAACGAAACACAACTA	906
Qy	1021	ACTAGGAAATTTATATACAGATCCAGTGGG	1049
Db	907	ACAGGGAAGTATATACAGATCCACTGGG	935
RESULT 6			
US-11-108-389-1			
: Sequence 1, Application US/11108389			
: Publication No. US20050261188A1			
: GENERAL INFORMATION:			
: APPLICANT: Andre R. Abad			
: APPLICANT: Ronald D. Flammagan			
: APPLICANT: Rafael Herrmann			
: APPLICANT: Theodore W. Kahn			
: APPLICANT: Albert L. Lu			
: APPLICANT: Billy Fred McCutchen			
: APPLICANT: James K. Presnail			
: APPLICANT: James F.H. Wong			
: TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal			
: FILE OF INVENTION: Activity			
: FILE REFERENCE: 35718/291049			
: CURRENT APPLICATION NUMBER: US/11/108,389			
: CURRENT FILING DATE: 2005-04-18			
: PRIOR APPLICATION NUMBER: 60/391,786			
: PRIOR FILING DATE: 2002-06-26			
: PRIOR APPLICATION NUMBER: 60/460,787			
: PRIOR FILING DATE: 2003-04-04			
: PRIOR APPLICATION NUMBER: 10/606,320			
: PRIOR FILING DATE: 2003-06-25			
: NUMBER OF SEQ ID NOS: 134			
: SOFTWARE: FastSeq for Windows Version 4.0			
: SEQ ID NO 1			
: LENGTH: 3621			
: TYPE: DNA			
: ORGANISM: Bacillus thuringiensis			
: FEATURE:			
: NAME/KEY: CDS			
: LOCATION: (1)...(3621)			
: FEATURE:			
: NAME/KEY: misc_feature			
: LOCATION: (0)...(0)			
: OTHER INFORMATION: CRY1218-1			
: US-11-108-389-1			

Query Match 4.9%; Score 105; DB 7; Length 3621;
Best Local Similarity 53.1%; Pred. No. 1.9e-15;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

QY 421 GCACTTCTATATGATTTAGTATCTATATCTGTAAGAGGAGAGAGGCTGTTA 480
DB 337 GAAATTTTATGCAACAAGTAGAAGAACTCATTAATCAAAAATAGCAATATGCAAG 396
QY 481 AGTGACGGGGTTCAGATTTTGAAGGTGAATGACCTGTTATCAAGATTAATCTTCAT 540
DB 397 AATTAACGGCTTCGGAATTAAGAGATTTGATTAATTAACCA---TATATCTACT 453
QY 541 TATCTTGAGATTTGGCTTACAGATAATCAATCTTAATAAACTTGCTGACGTATTA 600
DB 454 GCGCTTGAGAAATGGGAAGAAATCCAAATGTTCAAGACCTTACAGATGTCGAAAT 513
QY 601 CAGTTCCAGACGGGGAAGAAATTTGACTTAATCTTTACAGGCTATTAACAGACAG 660
DB 514 CGATTTGAAATCTGGATAGTTTATTTACGCAATATATGCCA---TCTTTAGAGTGACA 570
QY 661 AAAGCTGAAATATATTTATTTGCTACGTATGTCAGACTGCAATGTCATTTTACTA 720
DB 571 AATTTTGAAGTACATTCCTTACTGTATATGCAATGCGACCAACTTCACTTACTGTTA 630
QY 721 TTAAGGAGCGCATTAATAATTAATAAAGAAATGGGAGCTAGTGTCCACCGTTGTATCA 780
DB 631 TTAAGGAGCGCTCAATTTTGTGAGAGAAATGGGGA-----TGGTCA 672
QY 781 GGGTCAGGAGAACTGATTTGTAACGAGCGGTTAAACGAAATTAAGATATCTAT 840
DB 673 ACAACTACTATTAATACTATTAATGATCGTCAATGAACTTACGTGCAATATTCGAT 722
QY 841 TATTTGTAGGGTGTGTAACAAGGTTTATGATCAGATTAAGACGCGGGTACAGTCT 900
DB 733 CACTGTGTAAAGTGATGTAACGCTTTTACCAAAATTTAAA-----GGCAGAGCGCT 786
QY 901 GAACTTGTGCGAATTTAATAATTTCTGAGAAATGACGTTGGCGGTATGATATTT 960
DB 787 AAACAATGGGTGACATTAACCAATTCGTAGAGAAATGACACTGGCGTTTATGATGTT 846
QY 961 ATTGCTATTTTCCACTTATGATTTGAAAAATATCATTAAGCAAGTGTAGATTA 1020
DB 847 GTTGCACTTATTTCCCAATTTTACACACGCACTGACCAATGGAAGCAACACTA 906
QY 1021 ACTAGGAAATTTATACAGATCCAGTGG 1049
DB 907 ACAAGGAAATTTATACAGATCCACTGG 935

RESULT 7
US-11-058-727-17
; Sequence 17, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F. H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058.727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04

PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4874
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Genomic DNA 1218-1
US-11-058-727-17

Query Match 4.9%; Score 105; DB 7; Length 4874;
Best Local Similarity 53.1%; Pred. No. 2.2e-15;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

QY 421 GCACTTCTATATGATTTAGTATCTATATCTGTAAGAGGAGAGAGGCTGTTA 480
DB 1067 GAAATTTTATGCAACAAGTAGAAGAACTCATTAATCAAAAATAGCAATATGCAAG 1126
QY 481 AGTGACGGGGTTCAGATTTTGAAGGTGAATGACCTGTTATCAAGATTAATCTTCAT 540
DB 1127 AATTAACGGCTTCGGAATTAAGAGATTTGATTAATTAACCA---TATATCTACT 1183
QY 541 TATCTTGAGATTTGGCTTACAGATAATCAATCTTAATAAACTTGCTGACGTATTA 600
DB 1184 GCGCTTGAGAAATGGGAAGAAATCCAAATGTTCAAGACCTTACAGATGTCGAAAT 1243
QY 601 CAGTTCCAGACGGGGAAGAAATTTGACTTAATCTTTAGCAGGCTATTAACAGACAG 660
DB 1244 CGATTTGAAATCTGGATAGTTTATTTACGCAATATATGCCA---TCTTTAGAGTGACA 1300
QY 661 AAAGCTGAAATATATTTATTTGCTACGTATGTCAGACTGCAATGTCATTTTACTA 720
DB 1301 AATTTTGAAGTACATTCCTTACTGTATATGCAATGCGACCAACTTCACTTACTGTTA 1360
QY 721 TTAAGGAGCGCACTTAATAATTAATAAAGAAATGGGAGCTAGTGTCCACCGTTGTATCA 780
DB 1361 TTAAGGAGCGCTCAATTTTGTGAGAGAAATGGGGA-----TGGTCA 1402
QY 781 GGGTCAGGAGAACTGATTTGTAACGAGCGGTTAAACGAAATTAAGATATCTAT 840
DB 1403 ACAACTACTATTAATACTATTAATGATCGTCAATGAACTTACGTGCAATATTCGAT 1462
QY 841 TATTTGTAGGGTGTGTAACAAGGTTTATGATCAGATTAAGACGCGGGTACAGTCT 900
DB 1463 CACTGTGTAAAGTGATGTAACGCTTTTACCAAAATTTAAA-----GGCAGAGCGCT 1516
QY 901 GAACTTGTGCGAATTTAATAATTTCTGAGAAATGACGTTGGCGGTATGATATTT 960
DB 1517 AAACAATGGGTGACATTAACCAATTCGTAGAGAAATGACACTGGCGTTTATGATGTT 1576
QY 961 ATTGCTATTTTCCACTTATGATTTGAAAAATATCATTAAGCAACAGTGTAGATTA 1020
DB 1577 GTTGCACTTATTTCCCAATTTTACACACGCACTGACCAATGGAAGCAACACTA 1536
QY 1021 ACTAGGAAATTTATACAGATCCAGTGG 1049
DB 1637 ACAAGGAAATTTATACAGATCCACTGG 1665

RESULT 8
US-11-108-389-17
; Sequence 17, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu

```
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnall
APPLICANT: James F. H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
FILE REFERENCE: 35718/291049
CURRENT APPLICATION NUMBER: US/11/108,389
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 4874
TYPE: DNA
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Genomic DNA 1218-1
US-11-108-389-17
```

Query Match 4.9%; Score 105; DB 7; Length 4874;
Best Local Similarity 53.1%; Pred. No. 2.2e-15;

Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

```
421 GCACCTTCATATGTATGATTAATCTATATTCGTAAAGAGGAGACGAGCGTGA 480
1067 GAAATTTTATGACACAGTAGAAGAACTATTATCAAAAATAGCAGATTCGCAAG 1126
481 AGTACGGGGTTGCAATTTTGAAGGTGAATGACCTGCTTATCAAGATTTATCTTCAT 540
1127 AATTAAGCGCTTCGGAATTAGAAGGATGATTAATTAACAA--TTATCTTAAGT 1183
541 TATCTTGAGATTTGGCTTAAGATTAATCAATCTTAAAACTTGCTGACGATGTTAA 600
1184 GCGCTTGAAAGATGGAGAAATCCAAATGTTCAAGACCTTACGAGATGCGCAAAAT 1243
601 CAGTTCACAGCAGGAGAAAGATTCCTAATCTTAACTTTAGCAGGGTCAATTAACAGCA 660
1244 CGATTTGAATCTCGATAGTTATTTACCAATATATGCCA---TCTTTAAGAGTACA 1300
661 AAAGCTGAATATTTATTTATGCTACGATATGCAAGCTGCAAAATGTCATTTATTA 720
1301 AATTTGAAGTACATTCCTTACTGATATGCAATGCGACCAACCTTCACTTACTGTTA 1360
721 TTAAGGAGCGCAGTTAATTAATAAAGAAATGGGAGCTAGTGTCCACCGTTGATCCA 780
1361 TTAAAGGACCGCTCAATTTTGGAGAAATGGGGA-----TGGTCA 1402
781 GGGTCAGGAGAACTGATTTGTAACGAGCGGTAAAGCGAAATTAAGAGTACTAAT 840
1403 ACACTACTATTTAATACTATTTATGATCGCAATGAACTTACTGCAAGATATTCGAT 1462
841 TATTTGTAGAGTGTATTAACAAGGTTTATGATCAGATTAAGACAGCGGTTACAGTGT 900
1463 CACTGTGTAAGGTATGAACTGTTTGAAGCAAAATTAATA-----GGCAGAGCGCT 1516
901 GAAGTTGGTCGAAATTTAATAATTTCTGAGAGAAATGACGTTGGCGGTATTGATATT 960
1517 AAACAAATGGGTGACATTAACCAATTCCTGAGAAATGACACTGGGCGTTTAAAGTGT 1576
961 ATTGCTATATTTCAACTTATGATTTTGAAGAAATATCCATTAGCAACAAGTGAAGTTA 1020
1577 GTTGCATATTTCCAAATTTATGACACGCACTGACCCATGGAAGAAAGCAACACTA 1049
1021 ACTAGGAAATTTATACAGATCCAGTGGG 1049
ACTAGGAAATTTATACAGATCCAGTGGG 1049
```

DB 1637 ACAAGGAAATATATACAGATCCAGTGGG 1665

RESULT 9

US-11-058-727-55

Sequence 55, Application US/11058727

Publication No. US20050261483A1

GENERAL INFORMATION:

APPLICANT: Andre R. Abad

APPLICANT: Ronald D. Flannagan

APPLICANT: Rafael Herrmann

APPLICANT: Theodore W. Kahn

APPLICANT: Albert L. Lu

APPLICANT: Billy Fred McCutchen

APPLICANT: James K. Presnall

APPLICANT: James F. H. Wong

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

FILE REFERENCE: 35718/287809

CURRENT APPLICATION NUMBER: US/11/058,727

PRIOR FILING DATE: 2005-02-15

PRIOR APPLICATION NUMBER: 60/391,786

PRIOR FILING DATE: 2002-06-26

PRIOR APPLICATION NUMBER: 60/460,787

PRIOR FILING DATE: 2003-04-04

PRIOR APPLICATION NUMBER: 10/606,320

PRIOR FILING DATE: 2003-06-25

NUMBER OF SEQ ID NOS: 134

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 55

LENGTH: 2019

TYPE: DNA

ORGANISM: Bacillus thuringiensis (mutated)

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(2019)

US-11-058-727-55

Query Match 4.7%; Score 101.8; DB 7; Length 2019;
Best Local Similarity 58.6%; Pred. No. 8.6e-15;

Matches 228; Conservative 0; Mismatches 137; Indels 24; Gaps 2;

```
661 AAAGCTGAATTTATTTATTTGCTACGATATGCAAGCGCAAAATGTCATTTATTA 720
583 AATTTGAAGTACATTCCTTACTGATATGCAATGCGACCACTTATTTACTGTTA 642
721 TTAAGGAGCGCAGTTAATTAATAAAGAAATGGGAGCTAGTGTCCACCGTTGATCCA 780
643 TTAAGGAGCGCTCAATTTTGGAGAAATGGGGA-----TGGTCA 684
781 GGGTCAGGAGAACTGATTTGTAACGAGCGGTAAAGCGAAATTAAGAGTACTAAT 840
685 ACACTACTATTTAATACTATTTATGATCGTCAAAATGAACTTACGCAAAATTTCTGAT 744
841 TATTTGTAGAGTGTATTAACAAGGTTTATGATCAGATTAAGACAGCGGTTCAAGTGT 900
745 CACTGTGTAAGGTATGAACTGTTTGAAGCAAAATTAATA-----GGCAGAGCGCT 798
901 GAAGTTGGTCGAAATTTAATAATTTCTGAGAGAAATGACGTTGGCGGTATTGATATT 960
799 AAACAAATGGGTGACATTAACCAATTCCTGAGAAATGACACTGGGCGTTTAAAGTGT 858
859 GTTGCATATTTCCAAATTTATGACACGCACTGACCCATGGAAGAAAGCAACAACCTA 918
961 ATTGCTATATTTCAACTTATGATTTTGAAGAAATATCCATTAGCAACAAGTGAAGTTA 1020
1021 ACTAGGAAATTTATACAGATCCAGTGGG 1049
919 ACAAGGAAATTTATACAGATCCAGTGGG 947
```

RESULT 10


```

APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flammagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnall
APPLICANT: James F. H. Wong
APPLICANT: Cao Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Acetylty
FILE REFERENCE: 35718/291049
CURRENT APPLICATION NUMBER: us/11/1,08,389
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/351,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55
LENGTH: 2019
TYPE: DNA
ORGANISM: Bacillus thuringiensis (mutated)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2019)
US-11-108-389-55

Query Match      4.7%; Score 101.8; DB 7; Length 2019;
Best local Similarly 58.6%; Pred. No. 8.6e-15;
Matches 228; Conservative 0; Mismatches 137; Indels 24; Gaps 2;

```

QY	661	AAAGCTGAATATATATATATAGTCCAGTAGTGCAGCTGCAATGTGCAATTTATTA	720
Db	583	AAATTTGAAAGTACCATCTTACTGTATATGCAATGAGCAACTTCAATTAAGTTA	642
QY	721	TTAAGGACGACGATTAAATATAAAAAGAAATGGGAGCACTAGTGTGTCCACCGTGTATCCA	780
Db	643	TTTAAAGSAGCGTCAATTTTGTGGAGAAAGATGGGA-----TGGTCA	684
QY	781	GGGTCAAGGAGAACTGATTTGTACGAGCGGTTAAAGCGAAATATAAGTATACTAAT	840
Db	685	ACAACACTATTTATATATCTATTTATGATCGTCAATATGAACCTTACTGCAAGATATCTGAT	744
QY	841	TATTTGTATGGGTGTATTAACAAGGTTTGATTCAGATAGAAGCGGGTAAACAAGTCT	900
Db	745	CACGTGTATAAGTGCGTATGAAACTGTGTTTAGCAAAATTTAAAA-----GGCAGAGCGCT	798
QY	901	GAAAGTTGTGCGAAATTTAATAAATTTCTGATAGAAATGACGTGGCGTATTTGATATTT	960
Db	799	AAACAATAGGGTGTACTATATACCAATTCCTGATAGAAATGACACTGGCGGTTTTATGATGTT	858
QY	961	ATTGCTATATTTCCACTTATGATTTGAAAAATATCCATTAGACAACAAGTATGAGTTA	1020
Db	859	GTTGCATTATTTCCCAATTATGACACANATACGTACCCAAATAGAAAGAAAGCAACAACTA	918
QY	1021	ACTAGGAAATTTATACAGATCCAGTGGG	1049
Db	919	ACAAGGAAAGTATATACAGATCCACTGGG	947

RESULT 12
 US-11-108-389-87
 ; Sequence 87, Application US/11108389
 ; Publication No. US20050261188A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andre R. Abad
 ; APPLICANT: Ronald D. Flannagan
 ; APPLICANT: Rafael Herrmann
 ; APPLICANT: Theodore W. Kahn


```

1 CURRENT APPLICATION NUMBER: US11/058,727
2 CURRENT FILING DATE: 2005-02-15
3 PRIOR APPLICATION NUMBER: 60/391,786
4 PRIOR FILING DATE: 2002-06-26
5 PRIOR APPLICATION NUMBER: 60/460,787
6 PRIOR FILING DATE: 2003-04-04
7 PRIOR APPLICATION NUMBER: 10/606,320
8 PRIOR FILING DATE: 2003-06-25
9 NUMBER OF SEQ ID NOS: 134
10 SOFTWARE: FastSeq for Windows Version 4.0
11 SEQ ID NO 91
12 LENGTH: 2019
13 TYPE: DNA
14 ORGANISM: Bacillus thuringiensis (mutated)
15 FEATURE:
16 NAME/KEY: CDS
17 LOCATION: (1)...(2019)
18 OS-11-058-727-91

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Query Match	4.7%	Score 100.2	DB 7	Length 2019;
Best Local Similarity	58.4%	Pred. No. 2.1e-14;		
Matches 227; Conservative	0;	Mismatches 138;	Indels 24;	Gaps 2

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Db	583	AAATTTGAAGTACATTCCTACTCTATATATGCAATGCAACCACTTCATTAC	642
Qy	721	TTAAGGACGCGATTAAATATTAATAAAGATGGGGACTAGTGTGTCCACCGTTAT	780
Db	643	TTAAAGGACGCGTCAATTTTGTGAGAAATGGGGA-----TGTC	684
Qy	781	GGGTCAAGGAGAACTGATTTGTACGAGCGGTTAAAGCGAAATATTAAGATTA	840
Db	685	ACAACTACTATTAATTAACCTATTATGATGTCAGAACTTACTGCAATATCT	744
Qy	841	TATGTGTAGGGTGTATTAACAGGGTTAGTCGATTAAGACAGGGGGTAA	900
Db	745	CACGTGTGAAGTGTATGAACTGCTTTGACAAATTTAAAH-----GGCAGCG	798
Qy	901	GAAGTTTGGTCGAATTTAATPAAATTTGTAAGAGAAATGAGTTGGCGTAT	960
Db	799	AAACAAATGGGTGACTATPACCAATTCGTTAGAAATGACACTGGGGTTTT	858
Qy	961	ATTGCTATTTTCCACTTATGATTTTGAATAATATTCATTAGCAACAAGTGA	1022
Db	859	GTTCATATATTCCAAATTAATGACAACTAACCTCAATGGAACGAAGCA	918
Qy	1021	ACTAGGGAATTTATACATCCAGTGGG	1049
Db	919	ACAAAGGAGATATATACATCCACTGGG	947

RESULT 15
 US-11-108-389-59
 Sequence 59, Application US/11108389
 Publication NO. US20050261186A1
 GENERAL INFORMATION:
 APPLICANT: Andre R. Abad
 APPLICANT: Ronald D. Flannagan
 APPLICANT: Rafael Herrmann
 APPLICANT: Theodore W. Kahn
 APPLICANT: Albert L. Lu
 APPLICANT: Billy Fred McCutchen
 APPLICANT: James K. Prensall
 APPLICANT: James F.H. Wong
 APPLICANT: Cao-Guo Yu
 TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
 Activity
 FILE REFERENCE: 35718/291049
 CURRENT APPLICATION NUMBER: US/11/108,389
 CURRENT FILING DATE: 2005-04-18
 PRIORITY APPLICATION NUMBER: 60/391,786
 PRIORITY FILING DATE: 2002-06-26

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? PRIOR APPLICATION NUMBER: 60/460,787
? PRIOR FILING DATE: 2003-04-04
? PRIOR APPLICATION NUMBER: 10/606,320
? PRIOR FILING DATE: 2003-06-25
? NUMBER OF SEQ. ID NOS: 134
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 59
? LENGTH: 2019
? TYPE: DNA
? ORGANISM: Bacillus thuringiensis (mutated)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)...(2019)
US-11-108-389-59

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Query Match	4.7%	Score 100.2	DB 7	Length 2019
Best Local Similarity	58.4%	Pred. No. 2,1e-14		
Matches 227, Conservative	0	Mismatches 138	Indels 24	Gaps 2

Qy	661	AAAGCTGAAATATATTATTTGCTTACCTATGTGCAAGCTGCAAAATGTGATTTATTTACTA	720
Db	583	AATTTGGAAGTACATCTCCTTACTGTAATATGCAATGCGACCAACTTCAATTACTGTGTA	642
Qy	721	TTAAGGAGCGCAGTTAAATATATAAAAAGATGGGAGCTAGTGTGCCAGCTGTGATCCA	780
Db	643	TTAAAGGACCGTCAATTTTGTGGAGAAATATGGGA-----TGTGCA	684
Qy	781	GGGTCAGGAGAACTGATTTGTATACGACCGGTTAAAGCGAAATTTAAAGATATATCTAT	840
Db	685	ACAATCACTTTTATATACTATTTATGATGTCGCAATGAAACTTACTGCGAATATTTCTGAT	744
Qy	841	TATTTGTAGGGTGTATTAACAAGGGTTTATGATCAGATTAAGACAGCGGGGTACAGTCT	900
Db	745	CACGTGTAAAGTGATATGAAACGTGGTTTACAAATTTAAAA-----GGCAGACGCT	798
Qy	901	GAAATTGTGCGAATTTAATAAATTTTCGTAGAGAAATGACGTGGCGGTATTTGGATATT	960
Db	799	AAACAATGGGTGACTATTAACCAATTCGTATGAGAAATGACACTGGCGGTTTTATGATGTT	858
Qy	961	ATTGCTATATTTCCAACTTATGATTTTGGAAAAATATCCATTAGACACAACTGTATGAGTTA	1020
Db	859	GTTCGCTATTTCCCAATTTATGACACAATTAACGTATCCCAATGAGAAACGAAAGCACAACTA	918
Qy	1021	ACTAGGGAATTTTATCAGATCCAGTGGG	1049
Db	919	ACAAAGGAGATATATACAGATCCACTGGG	947

Search completed: December 19, 2005, 13:47:51
Job time : 205.901 secs

Page 100 (100.0)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 02:23:18 ; Search time 861.297 Seconds

(without alignments)
16597.955 Million cell updates/sec

Title: US-10-782-141-1

Perfect score: 2145
Sequence: 1 ttccaccaataataatgtt.....atagttatttaccatcaa 2145Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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2: geneseg1980s:*
3: geneseg1990s:*
4: geneseg2000s:*
5: geneseg2001as:*
6: geneseg2001bs:*
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10: geneseg2003bs:*
11: geneseg2003cs:*
12: geneseg2004as:*
13: geneseg2004bs:*
14: geneseg2005s:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2145	100.0	2145	13	ADR89413
2	2019	94.1	2019	13	ADR89414
3	2010	93.7	2010	13	ADR89416
4	855	39.9	5980	13	ADR89400
5	747.2	34.8	2082	13	ADR89401
6	739.8	34.5	2073	13	ADR89403
7	174	8.1	1983	3	AAZ93234
8	174	8.1	3837	3	AAZ93235
9	172.4	8.0	3471	2	AAV16515
10	172.4	8.0	3471	2	AAV16515 DNA encod
11	162.8	7.6	2407	4	AAZ02478
12	133.6	6.2	4391	14	AAZ02478 B. thurin
13	119.8	5.6	1959	4	AAZ02466
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15	118.4	5.5	2016	13	ADR89409
16	118.4	5.5	2049	13	ADR89407
17	118.2	5.5	3687	12	ADR89478
18	118.2	5.5	3932	2	AAZ064112
19	118.2	5.5	3932	2	AAZ09160

20	118.2	5.5	3934	2	AAZ95051
21	118.2	5.5	3934	2	AAZ6434
22	118.2	5.5	3934	2	AAV83927
23	117.6	5.5	1806	13	ADR89392
24	117.6	5.5	1890	13	ADR89390
25	117.6	5.5	2190	13	ADR89389
26	116.8	5.4	3684	2	AAV15222
27	116.8	5.4	3684	4	AAZ89221
28	116.8	5.4	3684	4	AAZ02489
29	113.4	5.3	2019	8	ABV93759
30	112.4	5.2	3687	4	AAZ8240
31	112.4	5.2	4173	4	AAZ02482
32	111.8	5.2	1897	2	AAV13118
33	111.8	5.2	1897	3	AAZ39905
34	111.8	5.2	1897	4	AAZ6983
35	111.8	5.2	2019	8	ABV93756
36	111.8	5.2	2019	8	ABV93757
37	111.8	5.2	3471	2	AAV16516
38	111.8	5.2	3471	2	AAZ83877
39	111.8	5.2	3471	4	AAZ02477
40	111.8	5.2	3474	2	AAZ19323
41	111.8	5.2	4344	2	AAZ06782
42	111.8	5.2	4344	2	AAV99986
43	110.2	5.1	2019	8	ABV93758
44	107.8	5.0	2190	4	AAZ04855
45	107.8	5.0	2965	2	AAZ06636

ALIGNMENTS

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RESULT 1
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AC ADR89413;
XX
DT 18-NOV-2004 (first entry)
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DE AXMI-008 full length coding sequence.
XX
KW se; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
XX
OS Bacillus thuringiensis.
XX
FH Key
FH CDS
FT 127..2145
FT /*tag= a
FT /product= "AXMI-008"
FT /transl_except= pos:127..129, aa:Met
XX
XX W02004074462-A2.
XX
XX 02-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005829.
XX
XX 20-FEB-2003; 2003US-0448632P.
XX 20-FEB-2003; 2003US-0448633P.
XX 20-FEB-2003; 2003US-0448797P.
XX 20-FEB-2003; 2003US-0448806P.
XX 20-FEB-2003; 2003US-0448810P.
XX 20-FEB-2003; 2003US-0448812P.
XX 19-FEB-2004; 2004US-00781979.
XX 19-FEB-2004; 2004US-00782020.
XX 19-FEB-2004; 2004US-00782096.
XX 19-FEB-2004; 2004US-00782141.
XX 19-FEB-2004; 2004US-00782570.
XX 19-FEB-2004; 2004US-00783417.
XX
```

```
AAZ95051 DNA encod
AAZ6434 CRYETs ge
AAV83927 DNA encod
ADR89392 AXMI-004
ADR89390 AXMI-004
ADR89389 AXMI-004
AAV15222 Bacillus
AAZ89221 Bacillus
AAZ02489 B. thurin
ABV93759 B. thurin
AAZ8240 Nucleotid
AAV13118 Bacillus
AAZ39905 truncated
AAZ6983 Coding se
ABV93756 Bacillus
ABV93757 B. thurin
AAV16516 DNA encod
AAZ83877 Bacillus
AAZ02477 B. thurin
AAZ19323 CRY9C Cod
AAZ06782 Insectici
AAV99986 Nucleotid
ABV93758 B. thurin
AAZ04855 Bacillus
AAZ06636 Gene enco
```

PA (ATHE-) ATHENIX CORP.
XX
XX Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;
XX MPI, 2004-635574/61.
DR P-PSDB; ADR89415.
XX
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
XX Claim 1; SEQ ID NO 25; 178bp; English.
XX
XX This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start frame.
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX
XX Sequence 2145 BP; 710 A; 338 C; 441 G; 656 T; 0 U; 0 Other:
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Query Match 100.0%; Score 2145; DB 13; Length 2145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 TTTACCAAAATATATATGTTTTTTTGTAGAAAATGTTTACAGAAATACATGGGGTACTA 60
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DB 61 CGAATATATAGAAAGACCTGGCATATATTTTATGAGTCTCTTAAAAAATAGGACTATA 120
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DB 121 TAAAGAGTGAATAATGAAATCTTATCAAAATCAAAATGATGAAATTCGATGGT 180
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DB 241 CCTATTAACCTGACGCTTGTCAGGAAGCCATGCGAATACGTGGAAATAGTCTCG 300
QY 301 GATATAGTACTATTTGGGACATACCTTATCAATTTCTTGCTAGAACCCGGTATAGGTGA 360
DB 301 GATATAGTACTATTTGGGACATACCTTATCAATTTCTTGCTAGAACCCGGTATAGGTGA 360
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DB 361 ATTCTGTAATATTTTCAATATTAACAAACCTCATTCCTTCTGCTCAATCTGTGGCA 420
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QY 481 AGTACGCGGGTTCAGATTTTGAAGGTGAATGCTCTATCAAGATTTATCTTCAT 540
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DB 541 TATCTTGAGGATTTGGCTTACAGATTAATCAAAATCTTAAAAAACTTGCTGACGTAGTAA 600

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DB 601 CAGTTCGAAGCAGCGGGAAGAAAGATTCTTAACCTTTAGCAGGGCTATATCAAGACAG 660
QY 661 AAAGCTGAATAATTTATTTGCTACGTATGTCAGAGCTGCAATATGCTATTTACTA 720
DB 661 AAAGCTGAATAATTTATTTGCTACGTATGTCAGAGCTGCAATATGCTATTTACTA 720
QY 721 TTAAGGACGCGATTAAATATTAAGAAATGGGACTAGTGTGTCACCGTTGATCCA 780
DB 721 TTAAGGACGCGATTAAATATTAAGAAATGGGACTAGTGTGTCACCGTTGATCCA 780
QY 781 GGGTACGAGGAGACGTATTTGTAACGAGGGTTTAAAGGAAATTAAGATATCTAT 840
DB 781 GGGTACGAGGAGACGTATTTGTAACGAGGGTTTAAAGGAAATTAAGATATCTAT 840
QY 841 TATTTGTAGGGTGTATTAACAAGGTTTATGATCAGATTAAGACAGCGGGTACAGTGT 900
DB 841 TATTTGTAGGGTGTATTAACAAGGTTTATGATCAGATTAAGACAGCGGGTACAGTGT 900
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QY 1321 ATTTATTTCAATTAGCTAGATATGCAATGCAACCGTTTGGGTATTCATCCACGGGCAT 1380
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DB 1681 TATGACAGAGGTACGTACACGCTGGCGCTTATACAGAGAGATGTAGTAACTTA 1740
QY 1741 CCTATACAGAGATTTAAAAATACGTTAACTTCTGACACCGAATTAATAATACCGT 1800
DB 1741 CCTATACAGAGATTTAAAAATACGTTAACTTCTGACACCGAATTAATAATACCGT 1800
QY 1801 GTTAGACTTCGCTACGCGAGTGGAGACCTTGCTCCGATGAGAAAGATGCTGCCA 1860
DB 1801 GTTAGACTTCGCTACGCGAGTGGAGACCTTGCTCCGATGAGAAAGATGCTGCCA 1860
QY 1861 AGTTCTGTTCAATGCTAATTTTCTGCTCCACTACAGGTGCTATGATTTGAT 1920
DB 1861 AGTTCTGTTCAATGCTAATTTTCTGCTCCACTACAGGTGCTATGATTTGAT 1920
QY 1921 TATGACACACCTAGTAACTACATTAATCAATCAGGTGTGAATAATATACAAAT 1980
DB 1921 TATGACACACCTAGTAACTACATTAATCAATCAGGTGTGAATAATATACAAAT 1980
QY 1981 CTATCTGTTACCACTTATTTGTGACAAAGTCGAATTTATCCCAATTTGACATCAAAAT 2040
DB 1981 CTATCTGTTACCACTTATTTGTGACAAAGTCGAATTTATCCCAATTTGACATCAAAAT 2040
QY 2041 GAAAAATGTACGAATGTCAATTGGAAGGACATATGTAGATGTGAAGATCAATCC 2100
DB 2041 GAAAAATGTACGAATGTCAATTGGAAGGACATATGTAGATGTGAAGATCAATCC 2100
QY 2101 TTGGAACCAAAAAAGATGTGAATAGTTATTTATTTATTTATTTATTTATTTA 2145
DB 2101 TTGGAACCAAAAAAGATGTGAATAGTTATTTATTTATTTATTTATTTATTTA 2145

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RESULT 2
ID ADR89414 standard; CDNA; 2019 BP.
AC ADR89414;
DT 18-NOV-2004 (first entry)
XX
DE AXMI-008 coding sequence.
XX
KM ss: gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KM expression cassette; transformation; transgenic plant; bacteria;
KM lepidoptera; coleoptera; pest; pesticide; resistance;
XX
OS Bacillus thuringiensis.
XX
FX Key Location/Qualifiers
FH CDS 1..2019
FT /*tag= a
FT /product= "AXMI-008"
FT /transl_except= pos:1..3, aa:Met
XX
PN MO2004074462-A2.
XX
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004US-00782570.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-0078197P.
PR 19-FEB-2004; 2004US-0078209P.
PR 19-FEB-2004; 2004US-0078206P.
PR 19-FEB-2004; 2004US-0078214P.
PR 19-FEB-2004; 2004US-00782570.

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PR 19-FEB-2004; 2004US-00783417.
XX
XX (ATHE-) ATHENIX CORP.
PA
XX
PI Carozzi N, Hargise T, Koziel MG, Duck NB, Carr B;
XX
XX WPI; 2004-635574/61.
DR
DR P-PSDB; ADR89415.
XX
XX
PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
XX Claim 1; SEQ ID NO 26; 178bp; English.
XX
XX
CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX
XX
SQ Sequence 2019 BP; 662 A; 324 C; 419 G; 614 T; 0 U; 0 Other;

Query Match 94.1%; Score 2019; DB 13; Length 2019;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTGAAAAATGTGAATTTCTTATCAAAATACAAATGATGAAATTTGATGTTCCCG 186
DB 1 GTGAAAAATGTGAATTTCTTATCAAAATACAAATGATGAAATTTGATGTTCCCG 60

QY 187 AATACACAAATATGTCAACAGATATCTTTGCAAAAGATCCAAATATATTTCCAT 246
DB 61 AATACACAAATATGTCAACAGATATCTTTGCAAAAGATCCAAATATATTTCCAT 120

QY 247 AACCTGACGCTTGTGAGGAGGACGATGCAAGATACGTGGAAATCAGTCTGGATATA 306
DB 121 AACCTGACGCTTGTGAGGAGGACGATGCAAGATACGTGGAAATCAGTCTGGATATA 180

QY 307 GTACTATTGGGACATACCTTATACAAATTTCTGTAACCCGGTATAGGTGAATTCCT 366
DB 181 GTACTATTGGGACATACCTTATACAAATTTCTGTAACCCGGTATAGGTGAATTCCT 240

QY 367 GTAAATTTTCAATATTAACAAACATCTCCGCTTCTGTAATCTGAGGAGACCT 426
DB 241 GTAAATTTTCAATATTAACAAACATCTCCGCTTCTGTAATCTGAGGAGACCT 300

QY 427 TCTATATGTATTAATATCTAATTAATTCGTAAGAGTGAAGACGAGACGGTTAAGTAC 486
DB 301 TCTATATGTATTAATATCTAATTAATTCGTAAGAGTGAAGACGAGACGGTTAAGTAC 360

QY 487 GGGGTTGACATTTTGAAGGCTGAATGACTGTTATCAAGATTATATCTTCAATATCTT 546
DB 361 GGGGTTGACATTTTGAAGGCTGAATGACTGTTATCAAGATTATATCTTCAATATCTT 420

QY 547 GAGGATTTGGCTTACAGTAATCAATCCGTAACAACTGCTGACGTAAGTAAACGTTCC 606
DB 421 GAGGATTTGGCTTACAGTAATCAATCCGTAACAACTGCTGACGTAAGTAAACGTTCC 480

QY 607 CAAGCAGGGAAGAGATTTCACTAACTTTAGCAGGGTCAATTAACAAGACGAAAGCT 666
DB 481 CAAGCAGGGAAGAGATTTCACTAACTTTAGCAGGGTCAATTAACAAGACGAAAGCT 540

QY 667 GAAATATTTATTTGCTACGTATGTGCAAGCTGCAAAAGTGCATTTATTTATTAAGG 726

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Db 541 GAAATATTATTTATGCTACGTATGTGCAAGTCGCAAAATGCAATTTACTATTAAAG 600
Qy 727 GAGCGATTAAATATATAAAAAGAAATGGGACCTAGTGTGTCCACCGTTGATCCAGGCTCA 786
Db 601 GAGCGATTAAATATATAAAAAGAAATGGGACCTAGTGTGTCCACCGTTGATCCAGGCTCA 660
Qy 787 GGGAGAACTGATTTGTAAACGAGCGTTTAAAGCGAAATATAAGATTAATTAATTTG 846
Db 661 GGGAGAACTGATTTGTAAACGAGCGTTTAAAGCGAAATATAAGATTAATTAATTTG 720
Qy 847 GTAGGTTGTATTAACAAGGTTTATAGATCAGATTAAGACAGCGGCTACAACTGTGAAGT 906
Db 721 GTAGGTTGTATTAACAAGGTTTATAGATCAGATTAAGACAGCGGCTACAACTGTGAAGT 780
Qy 907 TGGTCCAAATTTATTAATTTTCTGATGAGAAATGACGTGGCGGTATTTGATTTATTTGCT 966
Db 781 TGGTCCAAATTTATTAATTTTCTGATGAGAAATGACGTGGCGGTATTTGATTTATTTGCT 840
Qy 967 AATATTTCCAATATGATTTTGAATAATATCCATTAGCAACAAGTGTAGATTACTAG 1026
Db 841 AATATTTCCAATATGATTTTGAATAATATCCATTAGCAACAAGTGTAGATTACTAG 900
Qy 1027 GAAATTTATACAGATCCAGTGGGATATTCAGGGGAAATTTATGTTGGGAAACGTTT 1086
Db 901 GAAATTTATACAGATCCAGTGGGATATTCAGGGGAAATTTATGTTGGGAAACGTTT 960
Qy 1087 AGCTTTAATTCGGTATGAGAAAGCAATGGAACCGGGACCTGGTTAGTTACTTGGCTTCAA 1146
Db 961 AGCTTTAATTCGGTATGAGAAAGCAATGGAACCGGGACCTGGTTAGTTACTTGGCTTCAA 1020
Qy 1147 GCTATAGATATATATATAGTCAATTCATTAATCTTCAAGTTGGTATCTAGTGGCTGGGG 1206
Db 1021 GCTATAGATATATATATAGTCAATTCATTAATCTTCAAGTTGGTATCTAGTGGCTGGGG 1080
Qy 1207 GGAACCTGCTATTATGAGAACTTCAACAAGGGTAAACGGTCTTTTCAACGTATGTCTGA 1266
Db 1081 GGAACCTGCTATTATGAGAACTTCAACAAGGGTAAACGGTCTTTTCAACGTATGTCTGA 1140
Qy 1267 ACTACAGATTAATATCCACGTATATATTTTGGCAATCCGATATATTTAAATTAAT 1326
Db 1141 ACTACAGATTAATATCCACGTATATATTTTGGCAATCCGATATATTTAAATTAAT 1200
Qy 1327 TCATTAGCTAGATATGCAATGCAACCGTTTGGTGGATTCATTAATCCACGGACCTTGT 1386
Db 1201 TCATTAGCTAGATATGCAATGCAACCGTTTGGTGGATTCATTAATCCACGGACCTTGT 1260
Qy 1387 TCACTGTCAGAAATTTTCCGACAACTAAATACCTTCTGTATGAGGTAAACAGTTCT 1446
Db 1261 TCACTGTCAGAAATTTTCCGACAACTAAATACCTTCTGTATGAGGTAAACAGTTCT 1320
Qy 1447 GGGTACTCAGACAAATGGAATCTGTGTACAGATATTAATGAAGATCTACCACTAGT 1506
Db 1321 GGGTACTCAGACAAATGGAATCTGTGTACAGATATTAATGAAGATCTACCACTAGT 1380
Qy 1507 CGTACAAATATCTCTCATAGATTATCAATGCGGATGTGTCAAAAATGAACCTCCAG 1566
Db 1381 CGTACAAATATCTCTCATAGATTATCAATGCGGATGTGTCAAAAATGAACCTCCAG 1440
Qy 1567 GTTAACGATTTGGTGGACATACAGATATGAAAAAGATATTCGAATTTTATCCAGAT 1626
Db 1441 GTTAACGATTTGGTGGACATACAGATATGAAAAAGATATTCGAATTTTATCCAGAT 1500
Qy 1627 AAAATTAACGAATTTCTCGACAGTAAAGCTTTTCCCTTACAGACAGGTATACAGATATGCA 1686
Db 1501 AAAATTAACGAATTTCTCGACAGTAAAGCTTTTCCCTTACAGACAGGTATACAGATATGCA 1560
Qy 1687 GAGAGTTACGTCAACGCTGGGCTGTTTATACAGAGAGATGTAGTAACTTACCTTAT 1746
Db 1561 GAGAGTTACGTCAACGCTGGGCTGTTTATACAGAGAGATGTAGTAACTTATCTTAT 1620
Qy 1747 CAAGCAAGTTTAAATATACCTTTATCTTGCACCCACGAATTAATTAACCTGTATGA 1806
Db 1747 CAAGCAAGTTTAAATATACCTTTATCTTGCACCCACGAATTAATTAACCTGTATGA 1806
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Db 1621 CAAGCAAGTTTAAATATACCTTTATCTTGCACCCACGAATTAATTAACCTGTATGA 1680
Qy 1807 CTTCGCTACGCGAGGTGAGAGACCTGTCCGTTCCAGATAGAAAAAGATGGTCCGAAGTTCT 1866
Db 1681 CTTCGCTACGCGAGGTGAGAGACCTGTCCGTTCCAGATAGAAAAAGATGGTCCGAAGTTCT 1740
Qy 1867 GTTTCAAATATCTTATTTTCTGTCAGCTACAGGTGCTATAGTTCAATTTGATATGTG 1926
Db 1741 GTTTCAAATATCTTATTTTCTGTCAGCTACAGGTGCTATAGTTCAATTTGATATGTG 1800
Qy 1927 GACACCTTAGTTACTACATTTAATCAATCAGGTGTGAAATATTAATTAACAAATCTATCT 1986
Db 1801 GACACCTTAGTTACTACATTTAATCAATCAGGTGTGAAATATTAATTAACAAATCTATCT 1860
Qy 1987 GGTTCACCTTATTTGTGACAAAGTCCGAATTTATCCCAATGACATCCAAATTTGAAAA 2046
Db 1861 GGTTCACCTTATTTGTGACAAAGTCCGAATTTATCCCAATGACATCCAAATTTGAAAA 1920
Qy 2047 TGTACGAAATGTCAATTCGAAGAGACATATGTAGATGTGAAGAGTCAATCCTTGGA 2106
Db 1921 TGTACGAAATGTCAATTCGAAGAGACATATGTAGATGTGAAGAGTCAATCCTTGGA 1980
Qy 2107 AAAAAAAAAAGATTGTAAATATGTTTATTTATCAATTTAA 2145
Db 1981 AAAAAAAAAAGATTGTAAATATGTTTATTTATCAATTTAA 2019

RESULT 3
ADR89416
ID ADR89416 standard; cDNA; 2010 BP.
XX
AC ADR89416;
XX
AC 18-NOV-2004 (first entry)
XX
DE AXMI-008 alternative start site coding sequence.
XX
DE ss: gene: delta-endotoxin; delta-endotoxin associate polypeptide;
KM expression cassette; transformation; transgenic plant; bacteria;
KM lepidoptera; coleoptera; pest; pesticide; resistance;
XX pesticide activity.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT CDS 1..2010
FT FT /*tag= a
FT PN /product= "Alternative AXMI-008"
XX
XX MO2004074462-A2.
XX
PD 02-SEP-2004.
XX
XX 20-FEB-2004; 2004WO-US005829.
XX
XX 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX
XX (ATHE-) ATHENIX CORP.
PA Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;
XX
XX MPI; 2004-635574/61.
XX
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Db 1741 GCTAATTTCTCTCGTCAGGTACAGGTCCTATAGTTCAATTGATGTGACACCTTA 1800
Qy 1936 GTTACTACATTATATCAATCAAGTGTGAAATATTTATACAAATCTATGTGTTACAC 1995
Db 1801 GTTACTACATTATATCAATCAAGTGTGAAATATTTATACAAATCTATGTGTTACAC 1860
Qy 1996 CTATATGTGACAAAGTCGAATTTATCCCAATGACATCCAAATGMAAAATGACGAA 2055
Db 1861 CTATATGTGACAAAGTCGAATTTATCCCAATGACATCCAAATGMAAAATGACGAA 1920
Qy 2056 TGTCAATTCGAGAGACATATGTAGATGTGAAGAGTACATCTTGAAACAAAAA 2115
Db 1921 TGTCAATTCGAGAGACATATGTAGATGTGAAGAGTACATCTTGAAACAAAAA 1980
Qy 2116 GAGATGTAAATAGTTTATTTATCAATTA 2145
Db 1981 GAGATGTAAATAGTTTATTTATCAATTA 2010
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RESULT 4

ADR89400 standard; cDNA; 5980 BP.

AC ADR89400;

DT 18-NOV-2004 (first entry)

XX AXMT-008 full length coding sequence.

XX ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KM expression cassette; transformation; transgenic plant; bacteria;
KM lepidoptera; coleoptera; pest; pesticide; resistance;

XX Bacillus thuringiensis.

XX Key Location/Qualifiers

FH 168..2249

FT CDS /*tag= a

FT /product= "AXMT-008"

FT /transl_except= pos:168..170, aa:Met

XX PN W02004074462-A2.

XX PD 02-SEP-2004.

XX PF 20-FEB-2004; 2004MO-US005829.

XX PR 20-FEB-2003; 2003US-0448632P.

XX PR 20-FEB-2003; 2003US-0448633P.

XX PR 20-FEB-2003; 2003US-0448797P.

XX PR 20-FEB-2003; 2003US-0448806P.

XX PR 20-FEB-2003; 2003US-0448810P.

XX PR 19-FEB-2004; 2004US-00781979.

XX PR 19-FEB-2004; 2004US-00782020.

XX PR 19-FEB-2004; 2004US-00782141.

XX PR 19-FEB-2004; 2004US-00782570.

XX PR 19-FEB-2004; 2004US-00783417.

XX PA (ATHE-) ATHENIX CORP.

XX PI Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;

XX DR WPI; 2004-635574/61.

XX DR P-SDB; ADR89402.

XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.

PS Claim 1; SEQ ID NO 12; 178pp; English.

XX This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.

SQ Sequence 5980 BP; 2018 A; 976 C; 1146 G; 1840 T; 0 U; 0 Other;

Query Match 39.9%; Score 855; DB 13; Length 5980;

Best Local Similarity 71.4%; Pred. No. 2,3e-196;

Matches 1255; Conservative 0; Mismatches 430; Indels 72; Gaps 7;

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Qy 8 AATATATATGTTTTTTGTAGAAACATTTGTAACGAAATACATTTGGGTACTACGAATAT 67
Db 49 AATATATGAGTTTATTTGTAGAAACATTTGTAACGAAATACATTTGGGTACTACGAATAT 108
Qy 68 ATAGAAAGACACCTGGCATATTTTATAGTGTCTTAAATAATAGACTATATATAGAG 127
Db 109 ATAGAAAGACACCTAAACATATTTTATAGTGTCTTAAATAATAGACTATATATAGAG 168
Qy 128 TGAATAATATGAAATCTTATCAAAATATCAATATGATATGATGATGATGATGATGAT 187
Db 169 TGAATAATATGAAATCTTATCAAAATATCAATATGATATGATGATGATGATGATGAT 228
Qy 188 ATACACAAATATGTCAAACAGATATCTTTTGCAGAAAGATCCAAATATATTTCTATTA 247
Db 229 ATACACAAATATGTCAAACAGATATCTTTTGCAGAAATATGTCAGATATGTCAGATAT 288
Qy 248 ACCTGACGCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 307
Db 289 CTGGAATATGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 348
Qy 308 TAATATTTTCAATATATTAACAACTGATTCCTGCTAGAACCCGATATAGTGAATTCCTG 367
Db 349 CAAGTATTTGGATTAATCTTATAGAGTTTGTATAGAACCTGATTTGGGTGAATTAATA 408
Qy 368 TAATATTTTCAATATATTAACAACTGATTCCTGCTAGAACCCGATATAGTGAATTCCTG 427
Db 409 CACTATTTCAATATATTAAGAAACCTAATCCGACTAATGCTCAAACTGTGTGACACTTT 468
Qy 428 CTATATGATTTATGATCTATATATCTGTAAGAGGTATACGAGACCGTGTATAGAGAG 487
Db 469 CTATATGATTTATGATCTATATATCTGTAAGAGGTATACGAGACCGTGTATAGAGAG 528
Qy 488 GGGTTCAGATTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 547
Db 529 CGATTTCAAGTTTGTACCGGTAATTTGAAATATTTATGAGGATTTATCTTTCTTATCTTG 588
Qy 548 AGGATTTGCTTACAG-----ATAATCAATCTTAAATAAATCTTGACG 592
Db 589 GGGCTTGGCTTAAAGACGGTAAACCACTTCAAAAGCAATATATCTGATATGGAATAT 648
Qy 593 TAGTTAAACAGTTTCAAGACGGGAAAGATTTCTAAATCTTTTATAGACGGTCTATAT 652
Db 649 TAGTTATATATTTTAAACCTTCAAGAAAGATTTCAATGAATTTCTAGAGGGTCTATAT 708
Qy 653 CAAGACAGAAAGCTGAATATTTATTTGCTTACGATGATGCAAGCTGCAATATGATCAT 712
Db 709 CAAGAAACATGCTCAAGTATTTTATTTACTTCTTGTGACAAAGCTGCAATATGATCAT 768
Qy 713 TATTACTATTAAGGAGCGAGTTAAATATTAATAAAGATGGGAGCTAGTGTGCAACCGT 772
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Db      769 TATTACTATTAAAGGATGCACTGATATTAAGACAATGGTCCCATTTTGAAGTCAG 828
QY      773 TGTATCCAGGCTCAGGGAGAA-----CTGATTGTA 802
Db      829 AGAATGTAGAGTCCGAATTAATATCACCTAACAGTGTGTGATTTTACCGGTGATTAAT 888
QY      803 ACGAGCGTTTAAAGCGGAATAAAGATATCTAATTAATGTGTAGGGGTGATTAACA 862
Db      889 ATGAGCCATTAAATGCAAAACGGCAGATGATACCAATTAATGTTTAAATGATACAGG 948
QY      863 AGGCTTAGATCAGATTAAGACAGCGGATCAAGTGTGAAAGTTTGGTCGAAATTTATA 922
Db      949 TAGCTTTAAATCAGATTAATAAGGGGGGACAGGTGCTGACACTTGGTCGAAATTTATA 1008
QY      923 AATTTCGTAGAAATGACGTTGGCGGTATGATTAATTAATTTTCCAACTTAAG 982
Db      1009 AATTTCGTAGAAATGACGTTGGCGGTATGATTAATTAATTTTCCAACTTAAG 1068
QY      983 ATTTTGAATAATATCCATTAGCAACAAGTGTAGATTAATTAATTAATTAATTAATTA 1042
Db      1069 ATTTTGAATAATATCCATTGCAACACATGTAGAGTTGATAGGGAATTTATACAGATG 1128
QY      1043 CAGTGGATATATCAGGGGAAATTAATGTTGGGAACGGTTT-----TTAGCTTAAT 1096
Db      1129 CAGTGGATATATCAGGGAACTTAATGTTGGTTACGGAATTTGGCTTAATTAATTAATG 1188
QY      1097 CCGTAGAAGCAATATGAAACAGGGGACCTGTTAGTACTTGGCTTCAAGCTTAATTA 1156
Db      1189 GGTAGAGGCTTAATGAAACAGGGGACCTGTTAGTACTTGGCTTCAAGCTTAATTAATG 1248
QY      1157 TATTAAGTCACTTATTAATTTTCAAGTGTGTTATCTTAAGTGTGCGGGGAACTGCTC 1216
Db      1249 TATTAATGATATGTT-----TCGATATATTTTGGCGGCTGGGTAGGAATCTGCTC 1299
QY      1217 ATATGAAGCTTCAAAAGGTTAAGGTTCTTCAACGATATCTGGAACCTACGAGTA 1276
Db      1300 ATTAATGAAGCTTCAAAAGGTTAAGGTTCTTCAACGATATCTGGAACCTACGAGTA 1359
QY      1277 ATATGAAGCTTCAAAAGGTTAAGGTTCTTCAACGATATCTGGAACCTACGAGTA 1336
Db      1360 ATGATCTACGATATTAATTTTCAAGATGCCGATTAATTAATTAATTAATTAATTA 1419
QY      1337 GATATGAATGCAACCGTTTGTGGTATTAATCCACGAGCTTGTTCACGTCAG 1396
Db      1420 ---TCATGAACCTGTAGAGAGAGACTACCGCTACAGAGATATCGTTTCAAAAGCAG 1476
QY      1397 AATTTTTCGACAACTAAATATCTTCCGTATGAGTTAAACAGTTCTGGG---TACT 1453
Db      1477 ATTTTCGTAGGTTAGGGGACCTATTAATTAATTAATTAATTAATTAATTAATTAATTA 1536
QY      1454 CACAGCAATTTGATCTGTGTACAGGTTAATTAAGATCTTACCACTAGTCTGTAACA 1513
Db      1537 GAGTGAACAATTTGATCTGTGTACAGGTTAATTAAGATCTTACCACTAGTCTGTAACA 1590
QY      1514 ATTAATCTCATAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1573
Db      1591 GACCTCTCATAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1650
QY      1574 TATTTGTGTCACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1633
Db      1651 TATTTGTGTCACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1710
QY      1634 CGCAATTTCTGTCAGTAAAGCTTTTCCCTACAGAGGATCAGATTAATTAATTAATTA 1693
Db      1711 CACAAATTAACGGGGGTGAAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 1770
QY      1694 ACGTCAACGCTGGGCTT 1710
Db      1771 ATGTAAATTAAGGCACT 1787

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ID      ADR89401 standard; cDNA; 2082 BP.
XX
AC      ADR89401;
XX
XX      18-NOV-2004 (first entry)
XX
DE      AXMI-008 coding sequence.
XX
KW      ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW      expression cassette; transformation; transgenic; plant; bacteria;
KW      lepidoptera; coleoptera; pest; pesticide; resistance;
KW      pesticidal activity.
XX
OS      Bacillus thuringiensis.
XX
FH      Key
FH      CDS
FT      1.2082
FT      /tag= a
FT      /product= "AXMI-008"
FT      /transl_except= pos:1..3, aa:Met
XX
PN      W02004074462-A2.
XX
PD      02-SEP-2004.
XX
PE      20-FEB-2004; 2004MO-US005829.
XX
PR      20-FEB-2003; 2003US-0448632P.
PR      20-FEB-2003; 2003US-0448633P.
PR      20-FEB-2003; 2003US-0448797P.
PR      20-FEB-2003; 2003US-0448806P.
PR      20-FEB-2003; 2003US-0448810P.
PR      20-FEB-2003; 2003US-0448812P.
PR      19-FEB-2004; 2004US-00781979.
PR      19-FEB-2004; 2004US-00782020.
PR      19-FEB-2004; 2004US-00782096.
PR      19-FEB-2004; 2004US-00782141.
PR      19-FEB-2004; 2004US-00782570.
PR      19-FEB-2004; 2004US-00783417.
XX
PA      (ATHE-) ATHENIX CORP.
XX
PI      Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
XX
XX      WPI; 2004-635574/61.
XX
DR      P-PSDB; ADR89402.
XX
PT      New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT      and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT      for producing organisms with pesticide resistance.
XX
PS      Claim 1; SEQ ID NO 13; 178bp; English.
XX
XX
CC      This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC      endotoxin coding sequences of the invention have alternative start
CC      codons, producing more than one protein from a single open reading frame.
CC      The nucleic acid sequences of the invention are useful in DNA constructs
CC      or expression cassettes for transformation and expression in plants and
CC      bacteria. The nucleic acids and corresponding polypeptides are useful for
CC      killing lepidopteran or coleopteran pests. Compositions containing the
CC      delta-endotoxins of the invention, and methods for their production, are
CC      useful for the production of organisms with pesticide resistance,
CC      specifically bacteria and plants. These organisms are useful for
CC      generating altered or improved delta-endotoxin or delta-endotoxin-
CC      associated proteins that have pesticidal activity, or for detecting the
CC      presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC      nucleic acids in products or organisms.
XX
SQ      Sequence 2082 BP; 699 A; 305 C; 434 G; 644 T; 0 U; 0 Other;

```


[illegible]

QY 1642 CCGCAGTAAAGCTTTTGCCCTACAGCAGTACAGATATGACAGAGGTACGTACA 1701
DB 1543 CCGCGGTGAAAGAGTATTACTTCAAAATATCTGTAATGCTATACCTATATGAATA 1602
QY 1702 GCTGGGCTT 1710
DB 1603 AAAGCACT 1611

RESULT 7
AA293234 standard; DNA; 1983 BP.
XX
AC AA293234;
XX
DT 04-JUL-2000 (first entry)
XX
DE Sequence encoding truncated Cry9Aa toxin.
XX
KM Cry9Aa; insecticide; transgenic plants; pest control; crop protection;
de.
XX
OS Synthetic.
XX
OS Bacillus thuringiensis; ssp. galleria.
XX
FH Key Location/Qualifiers
FT CDS 17..1966
FT /tag= a
FT /product= "Cry9Aa toxin N-terminal fragment"

XX
PN MO200011025-A1.
XX
PD 02-MAR-2000.
XX
PF 24-AUG-1999; 99MO-FI000698.
XX
PR 24-AUG-1998; 98FI-00001809.
XX
PA (UNIC-) UNICROP LTD.
XX
PI Kuvshinov V, Kanerva A, Koiyu K, Pehu E;
XX
DR WPI; 2000-224660/19.
XX
DR P-PSDB; AAY83039.
XX
PT Modified synthetic DNA sequences comprise modification of the truncated
PT Cry9Aa gene of Bacillus thuringiensis for improved insect control in
XX
XX plants.
XX
PS Claim 2; Page 55-57; 90pp; English.
XX
CC Synthetic DNA sequences derived from the sequence of the truncated cry9Aa
CC gene of Bacillus thuringiensis ssp. galleria can be used for the
CC production of a unique insecticidal protein having the same properties as
CC the N-terminal domain of the insecticidal protein encoded by the native
CC cry9Aa gene of Bacillus thuringiensis ssp. galleria. The insecticidal
CC toxin works by binding to specific receptor molecules in the gut of
CC insects with consequent formation of ion channels in the epithelium. This
CC action leads to ion efflux and paralysis of the intestinal function,
CC which causes death of the insect. The synthetic DNA sequences exhibit
CC enhanced expression through improved mRNA processing, stability, and/or
CC translation providing improved tolerance against target insects. They can
CC be used in the production of transgenic plants capable of expressing the
CC N-terminal domain of the insecticidal protein encoded by the native
CC cry9Aa gene. They therefore have a role in pest control and crop
CC protection
XX
SQ Sequence 1983 BP; 626 A; 340 C; 387 G; 630 T; 0 U; 0 Other;

Query Match 8.1%; Score 174; DB 3; Length 1983;
Best Local Similarity 54.3%; Pred. No. 1.2e-31;
Matches 441; Conservative 0; Mismatches 335; Indels 36; Gaps 3;

QY 287 GGGAAATCAGTCTCGGATATAGTAATATGGGACATACCTTATACAAATCTTGCTAGAAC 346
DB 144 GCGATGACCAAAAGAGAGATATCTATTGGGACAAACCTATCTCTTATACAGCAC 203
QY 347 CCGGTATAGTGGAAATTCCTGTATATTTT-----CAATAATAAACAACTCAATCCGT 400
DB 204 CTTCTCTTACTGATTAATTTCAATAGTATATGACCTTATAGTAAAGTACTAGAGATA 263
QY 401 CTTCTGTATATCTGTGGACACTTCTATATGTGATTATAGTATCTATATATTCGTAAG 460
DB 264 GTAGTGAACATCCATATCAGATTTGTATATGTGACTATATATCTATATATGATTTAC 323
QY 461 AGGTAGACGAGCGGTGTAAGTACGCGGGTTCAGATTTTGGAGGTGAATATGACTGCTT 520
DB 324 GGGTATAGTACAGTGTTTTAAATGATGGGATTGCGAATTTTATATGTTCTGTACTTAT 383
QY 521 ATCAAGATTATATCTTC-----ATTATCTGAGGATTTGGCTTACAGATA 565
DB 384 ACAGAACTATTTAGAGGCTGTGATAGCTGGAATTAAGAAATCTTAATCTGCTGTGCTG 443
QY 566 AATCAATCTTAAAACTTGTGACGTATGTTAAACAGTCCAGACAGGAGGAAGATT 625
DB 444 AAGAACTCGTACTGTTTGAATTCGCGACTCAGAAATTTGATGAATTTTAACTCCGAG 503
QY 626 TCACTTAACTTTTACGAGGCTCATTATCAAGACAGAAAGCTGAATATTTATTTGCTTA 685
DB 504 GGTCTTAAAGCATGTGTGCTGTTAGCTAGACAAACAAATCCCAATATTTATTTACCTT 563
QY 686 CGTATGTGACAGCTGCAGATGTGCAATTTATCTATTTAAAGGACGCACTTAAATTAATA 745
DB 564 CTTTGGCAGCGCTGATTTTCCATTTATTTCTACTAAGGATGCTACTATAGATATGCGA 623
QY 746 AAGATGGGACTATGTTGTCCACCGTGTATCCAGGGTCAGGAGAACTGATTGTACG 805
DB 624 CTATTTGGGGGCTAATACATGCTACACCTTTATATA-----ATTATCAAT 668
QY 806 AGCGTTTAAAGCGAAATTAAGATTAATTAATTTGTAAGGAGTGTATTAACAAG 865
DB 669 CAAACTATGTAAGCTTATTTGAATCTATATCTATATTTGCTGATCTGATTTATTCGAG 728
QY 866 GTTATGATCAGATTAAGACAGCGGGTACAGTGTGTAAGTGTGTAATTTAATAAT 925
DB 729 GTTCAAGCACTAAGACAAAGAGGACATAGTGTACAGCTTGTTAGAAATTTCAATAGAT 788
QY 926 TTGTTAGAAATATGACGTTGGGCTATTTGATATTTTCTATATTTTCAACTATGATT 985
DB 789 ATCGTAGAGATGACATTTGATGTAATGATATGATGATCATATTTCAAGTCTTGATA 848
QY 986 TTGAATAATATCCATTAGACACAGTGTAGCTTAACTAGGGAATTTATACAGATCCAG 1045
DB 849 TTACTTAATTAACCATAGAAACAGATTTTCAAGTTAGTGGGTCAATTTATACGATCCAA 908
QY 1046 TGGGATATTCAGGGGGAATTTATGTTGGAA 1077
DB 909 TTGGTTTGTATGATGTAATGTAATGCTTAGGGA 940

RESULT 8
AA293235
ID AA293235 standard; DNA; 3837 BP.
XX
AC AA293235;
XX
DT 15-SEP-2003 (revised)
XX
DT 04-JUL-2000 (first entry)
XX
DE Sequence encoding native Cry9Aa toxin.
XX
KM Cry9Aa; insecticide; transgenic plants; pest control; crop protection;
de.
XX
OS Bacillus thuringiensis; ssp. galleria.

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XX Key Location/Qualifiers
FH 385..2364
FT /*tag= a
FT /product= "Cry9Aa toxin"
XX
XX WO200011025-A1.
XX
XX 02-MAR-2000.
XX
XX 24-AUG-1999; 99WO-FI000698.
XX
XX 24-AUG-1998; 98FI-00001809.
XX
XX (UNIC-) UNICROP LTD.
XX
XX Kuvshinov V, Kanerva A, Kolvu K, Pehu E;
XX WPI: 2000-224660/19.
XX P-PSDB; MAY82988.
XX
XX Modified synthetic DNA sequences comprise modification of the truncated
XX cry9Aa gene of Bacillus thuringiensis for improved insect control in
XX plants.
XX
XX Claim 10; Page 57-59; 90pp; English.
XX
XX Synthetic DNA sequences derived from the sequence of the truncated cry9Aa
XX gene of Bacillus thuringiensis ssp. galleria can be used for the
XX production of a unique insecticidal protein having the same properties as
XX the N-terminal domain of the insecticidal protein encoded by the native
XX cry9Aa gene of Bacillus thuringiensis ssp. galleria. The insecticidal
XX toxin works by binding to specific receptor molecules in the gut of
XX insects with consequent formation of ion channels in the epithelium. This
XX action leads to ion efflux and paralysis of the intestinal function,
XX which causes death of the insect. The synthetic DNA sequences exhibit
XX enhanced expression through improved mRNA processing, stability, and/or
XX translation providing improved tolerance against target insects. They can
XX be used in the production of transgenic plants capable of expressing the
XX C-terminal domain of the insecticidal protein encoded by the native
XX cry9Aa gene. They therefore have a role in pest control and crop
XX protection. (Updated on 15-SEP-2003 to standardise OS field)
XX
XX Sequence 3837 BP; 1279 A; 639 C; 791 G; 1128 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 174; DB 3; Length 3837;
XX Best Local Similarity 54.3%; Pred. No. 1,4e-31;
XX Matches 441; Conservative 0; Mismatches 335; Indels 36; Gaps 3;
XX
XX 287 GGGAAATAGTCTCGGATATAGTAATATGGGACATACCTTATCAATTCCTGCTAGAAC 346
XX |||||
XX 542 GCGATGACGCAAAAAGAGCAGATCTATTTGGGACACACATAGTCTCTTATACACAC 601
XX |||||
XX 347 CCGGTATAGGTGGAATCCGTATATTTT-----CAATATATAACAACTCATTCGCT 400
XX |||||
XX 602 CTCTCTTACTGATTAATTAATTAATAGTATAGACCTTATAGTAAGTAACTCTAGAGATA 661
XX |||||
XX 401 CTCTGCTCATCTGTGCGAGCACTTCTATATGTGATTTAGTATATATATGCTTAAG 460
XX |||||
XX 662 GTAGTGCACATCATATCATGATTTGCTATATGTGATTTATATATATATGATTTAC 721
XX |||||
XX 461 AGGTAGACGAGAGCGTGTAGTACCGGGTTCGATTTTGAAGGTGAATGACGCTT 520
XX |||||
XX 722 GGGTAAGTCAAGAGGTTTAAATGATGGATTCGAGATTTAAATGTTCTGTACTCTTAT 781
XX |||||
XX 521 ATCAAGATTAATTTCTTC-----ATTATCTTGAGGATTTGGCTTACAGATA 565
XX |||||
XX 782 ACGAGAACTATTTAGAGGCTCTGATAGTGAATTAAGAACTTAATTTGCTTCTGCTG 841
XX |||||
XX 566 AATCAATCTTAATAAACTTGCTGACGTAGTTAAACAGTTCCAAGCAGCGGAAGAGATT 625
XX |||||
XX 842 AAGAATCTCGTATCGTTTGAATCGCCGACCTCAGAAATTTGATAGAAATTTTAAACCGG 901
XX |||||

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QY 626 TCACTAACTTTTACGAGGCTCATTTACAGACAGAAAGCTGAATATTTATTTGCCCTA 685
DB 902 GGTCTTTAAAGAAATGGGCTCGTTAGCTAGACAAAATGCCCCAAATATTTATTTACCTT 961
QY 686 CGTATGCGAAAGCTGCAAAATGTGATTTATTTACTATTAAGGAGCGGATTAATATAA 745
DB 962 CTTTGGAGCGGCTGCAATTTTTCATTTATTTACTACTAAGGAGGCTACTAGATATGCA 1021
QY 746 AAGAATGGGAGCTAGTGTGTCCACCGTTGTATCCAGGCTCAGGAGAACTGATTTGAAC 805
DB 1022 CTATTTGGGGCTATATCAATGCTACACCTTTTATA-----ATTATCAAT 1066
QY 806 AGCGTTAAAGCGAAATTAAGAGTATTAATTTATTTGTTAGGCTGTATTAACAAG 865
DB 1067 CAAAACAGTAGAGACTTATGAACATAATATCTGATTTATTCGATATGTTATATATGAG 1126
QY 866 GTTTAGATCAGATTAAGCAGCGGCTACAGTCTGAAGTTTGGTGAATTTAATAAT 925
DB 1127 GTTTCACGCACTAAGCAAGAGGCACTAGTCTACAGCTTGTAGAAATTTCAATGAT 1186
QY 926 TTGATAGAGAAATGACGTTGGCGTATTTGATATTTATTTGCTATATTTCCAATATGATT 985
DB 1187 ATGCTAGAGAGATGACATTTATGATTTATGATATAGTATGATATTTCAAGTCTTATA 1246
QY 986 TTGAAAATATTCATTTAGCAACAAGTGTAGAGTTAACTAGGAAATTTATACAGATCCAG 1045
DB 1247 TTACTAATTTACCAATATGAACAAGATTTTCAGTTGAGTAGGCTATTTATACAGATCCA 1306
QY 1046 TGGATATTTACGAGGGAATTAATGCTTGGGAA 1077
DB 1307 TTGCTTTTGTACATCTGATGATGCTTGAAGGGA 1338

RESULT 9
AAV16515
ID AAV16515 standard; DNA; 3471 BP.
XX
XX AAV16515;
AC
XX
XX 11-JUN-1998 (first entry)
DT
XX
XX DNA encoding a Bacillus thuringiensis toxin designated 86Bb1 (a).
DE
XX
XX Toxin; lepidopteran pest; control; Agrotis ipsilon; black cutworm;
KM
XX
XX Heliothis virescens; Helicoverpa zea; ss.
XX
XX Bacillus thuringiensis.
OS
XX
XX Key Location/Qualifiers
FH 1..3471
FT /*tag= a
FT CDS
XX
XX NO9800546-A2.
XX
XX 08-JAN-1998.
PD
XX
XX 01-JUL-1997; 97WO-US011658.
PF
XX
XX 01-JUL-1996; 96US-00674002.
PR
XX
XX (MYCO) MYCOGEN CORP.
PA
XX
XX Schaepef HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
PI WPI: 1998-086971/08.
XX
XX P-PSDB; AAM46856.
XX
XX New isolated Bacillus thuringiensis isolate(s) - used to obtain genes
XX encoding toxins which are active against lepidopteran pests such as the
XX Black cutworm.
PS Example 5; Page 86-88; 183pp; English.
XX

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CC The present sequence is isolated from a *Bacillus thuringiensis* isolate
 CC (PS86B1). It encodes a toxin designated 86B1 (a) which is active against
 CC lepidopteran pests. The toxin isolates can be used for the control of
 CC lepidopteran pests such as *Agrotis ipsilon* (black cutworm), *Heliothis*
 CC *virescens* and *Helioverpa zea*. PCR primers and probes can be derived from
 CC the polynucleotide encoding the toxin and used for the amplification and
 CC detection of other toxin-encoding sequences
 XX

XX Sequence 3471 BP; 1144 A; 591 C; 734 G; 1002 T; 0 U; 0 Other;

Query Match 8.0%; Score 172.4; DB 2; Length 3471;

Best Local Similarity 54.2%; Pred. No. 3.4e-31;

Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 287 GGGAAATCAGTCTCGGATATAGTAACTTATGGGACATACCTTAATTCCTGCTAGAC 346
 DB 158 GCGATGACGAAAGAGAGAGATCTAATGGGACAAACATAGCTCTTATACAGCAC 217
 QY 347 CCGGTATAGGTGGAATTCCTGTAATTTT-----CAATAATAAACAACTCATTCCT 400
 DB 218 CTTCTCTTACTGATTAATTTCAATAGTATAGACCTTAATAGGTAAGTCTAGAGGTA 277
 QY 401 CTTCTGCTCATCTGTGGACGACCTTTATATGTGATTTAGTCTTAATTCGTAAG 460
 DB 278 GTAGTGACAAATCCATATCAGATTTGTCTATATGTGACTTATATCTAATTAATGATTTAC 337
 QY 461 AGGTAGACGAGAGCGGTATAGTACGCGGTGCAATTTTGAGGGTGAATACGCTT 520
 DB 338 GGGTAAGTCAAGATGTTTAAATGATGAGATGCAATTTAAATGTTCTGTACTCTTAT 397
 QY 521 ATCAAGATTATTAATCTTC-----ATTATCTTGAGATGGCTTACAGATA 565
 DB 398 ACAGGAATCTATTAGAGGCTCTGGATAGTGAATAGATCTTAATTCGCTTCTGCTG 457
 QY 566 AATCAAAATCTTAAAAAATTGCTGACGTAGTAAACAGTTCACAGCAGGGAAGAAAT 625
 DB 458 AAGAACTCCCTACTCGTTTAAATCGCCGACTCAGAAATTTGATAGATTTTAACCGAG 517
 QY 626 TCACATAACTTTAGCAGGGTCAATTATCAGACAGAAAGTGAATTTTATTTGGCTTA 685
 DB 518 GGTCTTTAAGCAATGGTGGCTCGTTAGCTAGACAAATGCGCAAAATATTAATTAACCTT 577
 QY 686 CGTATGTCAGAGCTGCAATATGTCATTTATTAATTAAGGACGCGATTAATTAATAA 745
 DB 578 CTTTGGAGCGGTGATTTTCCATTTATTAATTAAGGATAGTACTAGATTAAGGCA 637
 QY 746 AAGAAATGGGACCTAGTGTGTCACCGTTGATCCAGGGTCAGGAGAACTGATTGTAAG 805
 DB 638 CTAAATGGGGCTATCAATGCTACACCTTTTAA-----ATTATCAAT 682
 QY 806 AGCGGTTAAAGGGAATAAAGATATCTAATTAATTTGTAGGGTGTATTAACAG 865
 DB 683 CAAAATAGTAGAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 742
 QY 866 GTTATGATCAGATTAAGACAGCGGCTACAGTGTGCAAGTTGTCGAAATTAATAAT 925
 DB 743 GTTCAACGATTAAGACAGCGGCTACAGTGTGCAAGTTGTCGAAATTAATAAT 802
 QY 926 TTGTAAGAAATGACGTTGCGGTATTTGATTAATTAATTAATTAATTAATTAATTAAT 985
 DB 803 ATGTGATAGAGATGACATTTGATGTTATTAATTAATTAATTAATTAATTAATTAATTAAT 862
 QY 986 TTGAAATATTCATTAAGCAACAGTGTAGATTAATTAATTAATTAATTAATTAATTAAT 1045
 DB 863 TTACTAATTAATCCAAATGAAGAGATTTTCAAGTTGATGAGTGGTCAATTAATTAATTAAT 922
 QY 1046 TGGGATATTCAGGGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1077
 DB 923 TTGGTTTGTATCATGATAGTCTTAAGGGA 954

RESULT 10
 AAX83876

ID AAX83876 standard; DNA; 3471 BP.
 XX
 AC AAX83876;
 XX
 DT 09-SEP-1999 (first entry)
 XX
 DE *Bacillus thuringiensis* toxin 86B1 (a) encoding DNA.
 XX
 KW *Bacillus thuringiensis*; toxin; *Ostrinia nubilalis*; lepidopteran;
 KW European corn borer; black cutworm; ss.
 XX
 OS *Bacillus thuringiensis*.
 XX
 PN MO9393991-A2.
 XX
 PD 08-JUL-1999.
 XX
 PF 15-DEC-1998; 98WO-US026585.
 XX
 PR 31-DEC-1997; 97US-00002285.
 XX
 PA (MYCO) MYCOGEN CORP.
 XX
 PI Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
 PI Muller-Cohn J;
 DR WPI, 1999-405513/34.
 DR P-PSDB; AAT24959.
 XX
 PT Method for control of European corn borer using *Bacillus thuringiensis*
 PT toxins.
 XX
 PS Example 5; Page 90-92; 174pp; English.
 XX
 CC A method has been developed for the control of European corn borer
 CC (*Ostrinia nubilalis*), comprising contacting the pest with a pesticidal
 CC amount of a *Bacillus thuringiensis* toxin. The method is used for the
 CC control of European corn borer (*Ostrinia nubilalis*). The method can also
 CC be used for the control of other non-mammalian pests, particularly black
 CC cutworm, and other lepidopteran pests. The present sequence encodes a
 CC *Bacillus thuringiensis* toxin from the present invention
 XX
 SQ Sequence 3471 BP; 1144 A; 591 C; 734 G; 1002 T; 0 U; 0 Other;

Query Match 8.0%; Score 172.4; DB 2; Length 3471;

Best Local Similarity 54.2%; Pred. No. 3.4e-31;

Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 287 GGGAAATCAGTCTCGGATATAGTAACTTATGGGACATACCTTAATTCCTGCTAGAC 346
 DB 158 GCGATGACGAAAGAGAGAGATCTAATGGGACAAACATAGCTCTTATACAGCAC 217
 QY 347 CCGGTATAGGTGGAATTCCTGTAATTTT-----CAATAATAAACAACTCATTCCT 400
 DB 218 CTTCTCTTACTGATTAATTTCAATAGTATAGACCTTAATAGGTAAGTCTAGAGGTA 277
 QY 401 CTTCTGCTCATCTGTGGACGACCTTTATATGTGATTTAGTATCTAATTAATTCGTAAG 460
 DB 278 GTAGTGACAAATCCATATCAGATTTGTCTATATGTGACTTATATCTAATTAATTAATTAAT 337
 QY 461 AGGTAGACGAGAGCGGTATAGTACGCGGTGCAATTTTGAGGGTGAATTAATTAATTAATTAAT 520
 DB 338 GGGTAAGTCAAGATGTTTAAATGATGAGATGCAATTTTAATGTTTGTGACTCTTAT 397
 QY 521 ATCAAGATTATTAATCTTC-----ATTATCTTGAGATGGCTTACAGATA 565
 DB 398 ACAGGAATCTATTAGAGGCTCTGGATAGTGAATTAAGAAATCTTAATTTGCTTCTGCTG 457
 QY 566 AATCAAAATCTTAAAAAATTGCTGACGTAGTAAACAGTTCACAGCAGGGAAGAAAT 625
 DB 458 AAGAACTCCGTACTCGTTTAAATCGCCGACTCAGAAATTTGATAGATTTTAACCCGAG 517
 QY 626 TCACATAACTTTTAGAGGGTCAATTAATTAAGACAGAAAGCTGAATTAATTAATTAATTAAT 685


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Db      518 GGTCTTAAAGCAATGGTGGCTGCTTACGTAGACAAAATGCCAAATTTATTACTT 577
Qy      686 CGATGTGCAAGCTGCAAAATGTCATTATTACTATTAAAGGAGCAGTTAAATATAAA 745
Db      578 CTTTGGAGGGCTGCAATTTTTCATTATTACTAAGGAGTCTAATGATATGGCA 637
Qy      746 AAGATGGGACTAGTGTGTCCACCGTTGATCCAGGCTCAGGAGAACTGATTGTACG 805
Db      638 CTAATTTGGGGCTATACAAATGCTACACCTTTTATA-----ATTATCAAT 682
Qy      806 AGCGGTAAAAAGCAAAATATAAGATATACTAATTTGTTAGGGGTGATATAACAG 865
Db      683 CAAACTAGTAGAGCTTATTGAATCTATATCTGATTTATGGTCATTGGTATATGAG 742
Qy      866 GTTTAGATCAGATTAAGACAGGCGGCTCAAGTGTGTAAGTTGGTCCAAATTTATAAT 925
Db      743 GTTTCACGAACCTAAGCAACGAGGCACTGTGTACAGCTTGGTTGAATTTGATGAT 802
Qy      926 TTGCTAGGAATGACGTTGGCGGTATTGATATTATTTGCTATATTTCCAACTTATGAT 985
Db      803 ATCGTAGAGATACATTTGATGATTAATAGATAGATCAATTTTCAAGTCTGTATA 862
Qy      986 TTGAAAATATTCATTGCAACAGGTAGAGTTAAGGGAATTTATACAGATCCAG 1045
Db      863 TTACTAATTTACCAATAGAAACAGATTTTCAGTTGAGTAGGGTCAATTTATACAGATCAA 922
Qy      1046 TGGGATATTCAGGGGGAATTTATGTTGGGA 1077
Db      923 TTGGTTTGTATCATCTGATAGTCTTAGGGCA 954

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RESULT 11
ID AAS02478 standard; DNA; 2407 BP.

XX AAS02478;

DT 29-AUG-2001 (first entry)

XX B. thuringiensis DNA encoding a toxic crystal protein, CryET60.

XX Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
XX transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum;
XX sugarcane; tobacco; kapok; flax; potato; barley; turf grass;
XX pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
XX cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
XX cotton leaf perforator; CryET60; ds.

XX Bacillus thuringiensis.

XX Key Location/Qualifiers

FT CDS 1..2406

FT /*tag= a

FT /product= "CryET60"

FT /partial

FT /note= "No stop codon"

PN MO200119859-A2.

PD 22-MAR-2001.

PF 13-SEP-2000; 2000MO-US025361.

PR 15-SEP-1999; 99US-0153995P.

XX (MONS) MONSANTO CO.

XX Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;

XX WPI; 2001-281518/29.

XX P-PSDB; AAU02035.

PT Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
PT and the polynucleotides that encode them, useful for increasing the
PT insect resistance of plant.

XX Claim 17; Page 127-128; 173pp; English.

CC The sequence encodes a B. thuringiensis Lepidopteran-active delta-
CC endotoxin, crystal protein CryET60. The Lepidopteran-active B.
CC thuringiensis delta-endotoxin polypeptides may be used as compositions
CC that are applied to plant crops to protect them from insect damage. The
CC polynucleotides may be used in the production of transgenic plants that
CC express the insecticidal polypeptides and consequently have improved
CC insect resistance compared to non-transformed plants. Monocytledonous or
CC dicotyledonous plants may be protected in this way, for example corn,
CC wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
CC tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
CC cotton leaf perforator and spruce budworm) may be affected by application
CC of the insecticidal polypeptides (full details given in specification)

XX Sequence 2407 BP; 785 A; 409 C; 495 G; 718 T; 0 U; 0 Other;

Query Match 7.6%; Score 162.8; DB 4; Length 2407;
Best Local Similarity 53.4%; Pred. No. 6.3e-29;
Matches 434; Conservative 0; Mismatches 342; Indels 36; Gaps 3;

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Qy      287 GGAATCAGCTCGGATATAGTAACTATTGGGACATCTTATATACATTCCTGTAGAAC 346
Db      158 GCAATGACGAAAGAAAGACGATATCTATTGGGACACCAATAGTCTCTTATACAGCAC 217
Qy      347 CCGATATAGGTGAATTCCTGTAATTTT-----CAATATATAACAACTCATTCGT 400
Db      218 CTCTCTTACTGATTAATTTCAATAGTATATAGCCTTATATAGAAAGTACTAGAGATA 277
Qy      401 CTTCGTCAATCTGTGGGACGACCTTCTATATGTATTTAGTATCTATATTTGCTAAG 460
Db      278 GTATGACAAATCATATACATGATTTGTCTATATGTGCTTATATATATGATTTAC 337
Qy      461 AGGTAGACGAGCGGTATTAAGTACCGGGGTGACATTTTGAAGGGAATGACTCTT 520
Db      338 GGGTATGCTCAGAGTCTTTTAAATGATGAGATTGCAATTTTAAATGTTCTGACTCTTAT 397
Qy      521 ATCAATATTTATCTTC-----ATTATCTTGAGATTTGCTTACAGATA 565
Db      398 ACAGAACTATTTAAGAGGCTGTGATAGCTGATTAAGATTCCTAATTCGCTTCTGCTG 457
Qy      566 AATCAATCTTAAAAAATTGCTGAGCTGATTTAAACGTTCCAGACGCGGAAGAGATT 625
Db      458 AAGAACTCCGCTACTCGTTTGAATCGCCGACTCAGAAATTTGATGATTTTAAACCGGAG 517
Qy      626 TCACTAACTTTTAGAGAGGCTCATATCAAGACGAAAGCTGAATTTATTTATGGCTA 685
Db      518 GGTCTTAAAGAAATGGTGGCTCTTACCTAGACAAAATGCCAAATATTTATTACTCTT 577
Qy      686 CGATGTGCAAGCTGCAAAATGTCATTATTACTATTAAAGGAGCAGTTAAATATAAA 745
Db      578 CTTTGGAGCGCTGCAATTTTTCATTATTACTAAGGAGTCTAAGATATGGCA 637
Qy      746 AAGATGGGACTAGTGTGTCCACCGTTGATCCAGGCTCAGGAGAACTGATTGTACG 805
Db      638 CTAATTTGGGGCTATACAAATGCTACACCTTTTATA-----ATTATCAAT 682
Qy      806 AGCGGTAAAAAGCAAAATATAAGATATACTAATTTGTTAGGGGTGATATAACAG 865
Db      683 CAAACTAGTAGAGCTTATTGAATCTATATCTGATTTATGGTCAATGGATATATGAG 742
Qy      866 GTTTAGATCAGATTAAGACAGGCGGCTCAAGTGTGTAAGTTGGTCCAAATTTATAAT 925
Db      743 GTTCAACCGAACTAAGCAACGAGGCTGATGCTACAGCTTGTGTAATTTCAATGAT 802
Qy      926 TTGCTAGGAATGACGTTGGCGGTATTGATATTATTTGCTATATTTCCAACTTATGAT 985

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Db	803	ATCGAGAGAGATGACATTGATGGCATTTAGAAATAGTACGATCATTTTCAAGTCTTGATA	862
Qy	986	TTGAAAAATATCCATTAGCAACAAGTGTAGAGTTACTACTAGGAAATTTATACAGATCCAG	1045
Db	863	TTACTAAATTTACCCATATAGAAACAGATTTTTCAGTTGAGTAGGCGTATTATACAGATCCAA	922
Qy	1046	TGGGATATTCCAGGGGAAATTTATGGTTGGGAA	1077
Db	923	TTGGTTTGTATCATTGTAGTGTGTTAGGGA	954
RESULT 12			
AE61394			
ID	AE61394	standard; DNA; 4391 BP.	
AC	AE61394;		
XX			
DT	11-AUG-2005	(first entry)	
XX			
DE	Bacillus thuringiensis Cry19Aa coding sequence, SEQ ID 4.		
XX			
KW	Insecticide; crystal protein; Cry19Aa; gene; db.		
XX			
OS	Bacillus thuringiensis.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	719..2665	
FT		/tag= a	
FT		/product= "Cry19Aa"	
XX			
PN	US2005124803-A1.		
XX			
PD	09-JUN-2005.		
XX			
PF	30-AUG-2004; 2004US-00929754.		
XX			
PR	29-AUG-2003; 2003US-0498826P.		
XX			
XX	(OHIS) UNIV OHIO STATE RES FOUND.		
PA			
XX			
PI	Dean DH, Abdullah MA;		
DR	WPI: 2005-417057/42.		
DR	P-PSDB; AE61393.		
DR	EMBL; Y07603.		
XX			
XX	New modified Bacillus thuringiensis insecticidal crystal proteins (i.e.		
PT	Cry4Ba and Cry19a) with enhanced toxicity, useful for reducing or		
PT	eliminating populations of target insects (i.e. mosquitoes) that are		
PT	vectors of disease.		
XX			
PS	Disclosure; SEQ ID NO 4; 63bp; English.		
XX			
CC	The present invention relates to modified insecticidal Bacillus		
CC	thuringiensis crystal proteins Cry4Ba and Cry19a which have enhanced		
CC	toxicity against a variety of insects, e.g. mosquitoes and lepidoptera.		
CC	The modified proteins are useful for reducing or eliminating populations		
CC	of target insects that are vectors of disease, particularly mosquitoes.		
CC	The present sequence is the coding sequence of the wild-type Cry19a		
CC	protein, which can be modified with: a substitution of amino acids at		
CC	positions 355 through 358 with amino acids tyrosine, glutamine, aspartic		
CC	acid, and leucine; an insertion of at least one amino acid (e.g.		
CC	arginine) after position 358 and a deletion of the amino acids at		
CC	positions 414 through 418.		
XX			
SQ	Sequence 4391 BP; 1557 A; 630 C; 914 G; 1290 T; 0 U; 0 Other;		
Query Match 6.2%; Score 133.6; DB 14; Length 4391;			
Best Local Similarity 48.1%; Pred. No. 9e-22;			
Matches 720; Conservative 0; Mismatches 704; Indels 74; Gaps 9;			
QY	666	TGAATATATTATTGCTAGCTATGTGCAAGCTGCAAAATGTCATTTATTACTATTAAAG	725

Db	1303	TGAGTACTTTTATGCTGCTCTATGACACAAATTGGCAATCTGCATTTACTTTATTTACG	1362
Qy	726	GGAGCAGTTTAAATATATAAAAAGATGGGGACAGTGTGTCCACCGTTGTATCCAGGGTC	785
Db	1363	GGATGCTCAGATTTATGAGATTAATGTGTGAGCGCACG-----AGCTAA	1407
Qy	786	AGGAGAACTGATTTGTAAACGACGGTTTAAAAAGCAAAATTAAGAAGTATCTAATTTTG	845
Db	1408	TGCTCGGATATATTTATTCAMATATCAATTAGAAAAACAAGAAATATTCAGAAATATTG	1467
Qy	846	TGTAGGGGTGATATACAAGGGTTTATGATCGATTAAGACAGCGGGTCAAGTGTGAGT	905
Db	1468	TATTAATTTGGTATATATAGGCTTTTAAATGATTTTGAACGACAGGTAA-----	1516
Qy	906	TTGTGCAAAATTTATATAAATTTTGTGAGAAATGACGTTGGCGTATTTGATATATTATGC	965
Db	1517	-TGGSTAACTTTATATGCTTATGCTAGAGAAATGACTTACTGTATATGATATATTATTC	1575
Qy	966	TATATTTTCCAATTATGATTTTGAAAAATTCATTAGCAACAAGTATAGTTAACTAG	1025
Db	1576	AATGTCTCCATTTTATGACCGAGATTTATCTTACAGAAATTAAMAAACCAACTAACAG	1635
Qy	1026	GGAATTTTATACAGATCCAGTGGGATTTTCAGGGGGAAATTAATGTTGGAGCGGTTTT	1085
Db	1636	GGAATTTTATTCAGAT--GTTATTAATGGGAGATATATGACTTATGACTCTTATTT	1692
Qy	1086	TAGCTTTAATTCGTAGAGCAAAATGGAACACGGGGACCTGTATTAGTTACTTGCTTCA	1145
Db	1693	TTCTTTTGAGAAAGCTGATATCATCTTTATACAAAGGACCCCATCTCTTCACTGGCTAA	1752
Qy	1146	AGCTATAGATATATATGTCTATTTAATCTTGAGCTTGTTATCTTAGTGCTGGG	1205
Db	1753	AGGATTTTCGATTTGTAAACCAATCTATTTCTTATTTGACATTTTATCAGGTGTCAMAA	1812
Qy	1206	GGGAACCTGCTATATATAGACCTCAACAAGGGTAAGGTCCTTTTCAAGTATGTCTG	1265
Db	1813	TTAGTATTTCTTATCTATATATATTTTGTATTTAACGAGGGCTCTTTTAGGGACAGCAC	1872
Qy	1266	AACATCAGATATATATCCAGTATATATTTTTT---GGCAATACCGATATATTTTAAAT	1322
Db	1873	AGATTAATGTGGGACTTCTCTACATTAATATTTCCATCAAAATTCGATGTATATATTT	1932
Qy	1323	TATTTCAATTAGCTAGATATGCAATGCAACGTTTGTGGTATTC--ATCCACGGCA	1379
Db	1933	ATGACCGGAATATGAAATATATTTATCTTGGGGTGATCTGTAAATATTCAAAAAT	1992
Qy	1380	TCTTGTTCACAGTCGCAAAATTTTTCCGACAACCTAATAACTTCTCTATAGAGTAA	1439
Db	1993	GAAATTTTCTGTATCAGATATATATTTCTTCAAAAAGATTAATTAATGTGTCACACAGAC	2052
Qy	1440	CAGTTCTGGGTACTCAGACCAATTTGAATCTGTGTCCAGGTATATATAGATTCACC	1499
Db	2053	GAAATTAACCTGTGTGGACAGATTTTGATTTTTCTCACTAATTAAGAGGAAGTGAATT	2112
Qy	1500	ACCTAGTCGTAACAATTACTCTCATATGATTAATCAAAATGCGCATGTGTCAAA-----	1553
Db	2113	AGCAAAATATATGATTAATATCATATTTATCTATATGTATTAATGAGGGAACGTT	2172
Qy	1554	---TGAACCTCCAGAGTTAACGATTTGGTTGGACATATCAAGTATGAAAAAAGTTAA	1610
Db	2173	TGGTCAGAAACGTATGTTATTTGTTGCTTTTACACATATAGTGTTCATCTTAATAA	2232
Qy	1611	TGCAATTTATCCAGATTAATAATTACGAAATTCCTGCGATTAAGCTTTTGCCCATCAGC	1670
Db	2233	TACATTTTGACCGAATTAATAATGCAAAATTCCTGTATGAAGCTTCGAGTATTAATGG	2292
Qy	1671	AGGTACAGATATGACAGAGGTTATCTGTCAGACTGGGCTGTATTATCAGAGAGAGTGT	1730
Db	2293	ATGATTTTCAATTGAAAAAGST-----CCGGATTTACGGAGGAGATTT	2337
Qy	1731	AGTAACTTACCTTATCAAGCAAGTTTAAAAATACGTTTAATCTTGCACCCACGAATTA	1790
Db	2338	GGTAAAGTATGAGACAAATTCAGGTTTAACTATGCTTTTAAAGCTGAATTAATTAAGTTAA	2397

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QY 1791 AAATTACCGTGTGACTTCGCTACGGAGTGGAGACCTGGTCCGTTCCGAGTAGAAG 1850
DB 2398 AAAATATCGTGTGGAAATACGTTATTAATGTAACAGTCTAAATTAATTAACGAAA 2457
QY 1851 ATGG---TCGGCAAGTTCGTGTTCAAAATGCTAATTTTCTCGTCAGTCAAGGTGCTA 1907
DB 2458 ATGAAAAGGGAGAGATATATACACAAACAAATTCACAAATTTCTCCACATATGAGC 2517
QY 1908 TAGTTCAATTTGATTATGAGACACCTTAAGTACTACATTTATCAATCAGGTGTTGAAT 1967
DB 2518 CTTTCTTATTTAAGCTTTTACTATTAACAGCAAGAAAATATTTGATTTGACAAAT 2577
QY 1968 AATTATACAAATCTATCTGTTACCACTTATTTGTCACAAAGTCGAATTTATCCAAAT 2027
DB 2578 GAGAGTAACATATCCGTATGTTAGACAGTTTGTGAAGATATACATCTCTTATATAGA 2637
QY 2028 TGACATCCAAATTAAGAAAATGTACAAATGTCATTCGAAAGAGACATATGTAGATGTA 2087
DB 2638 TAAATCGAATTCCTCCCACTAATGATACATTCA-----GGAAATATGA 2686
QY 2088 AGAGTACAAATCCTTGGAAACAAAAGAGATTGTAATGTTATTTATCAATTA 2145
DB 2687 GGAATAATATGAAATTAAGAAAGATACAGAAACATTTAATGTAATTTGTTGATTA 2744

RESULT 13
AAS02466
ID AAS02466 standard; DNA; 1959 BP.
AC AAS02466;
XX
XX 29-AUG-2001 (first entry)
DE B. thuringiensis DNA encoding a toxic crystal protein, CryET43.
XX
XX Delta endotoxin; lepidopteran-active; crystal protein; insecticide;
KW transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum;
KW sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
KW pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
KW cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
KW cotton leaf perforator; CryET43; ds.
XX
XX Bacillus thuringiensis.
XX
XX Key Location/Qualifiers
FH 1. 1959
FT CDS /*tag= a
FT /product= "CryET43"
FT /partial
FT /note= "No stop or start codon"
XX
XX MO200119859-A2.
XX
XX PD 22-MAR-2001.
XX
XX PF 13-SEP-2000; 2000MO-US025361.
XX
XX PR 15-SEP-1999; 99US-0153995P.
XX
XX (MONS ) MONSANTO CO.
XX
XX Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;
XX
XX WPI: 2001-281518/29.
XX
XX P-PSDB; AAU02023.
XX
XX Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
PT and the polynucleotides that encode them, useful for increasing the
XX insect resistance of plant.
XX
XX Claim 17; Page 105; 173pp; English.
XX

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CC The sequence encodes a B. thuringiensis lepidopteran-active delta-
CC endotoxin, crystal protein CryET43. The lepidopteran-active B.
CC thuringiensis delta-endotoxin polypeptides may be used as compositions
CC that are applied to plant crops to protect them from insect damage. The
CC polynucleotides may be used in the production of transgenic plants that
CC express the insecticidal polypeptides and consequently have improved
CC insect resistance compared to non-transformed plants. Monocyledonous or
CC dicotyledonous plants may be protected in this way, for example corn,
CC wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
CC tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
CC cotton leaf perforator and spruce budworm) may be affected by application
CC of the insecticidal polypeptides (full details given in specification)
XX
SQ Sequence 1959 BP; 646 A; 348 C; 393 G; 572 T; 0 U; 0 Other;

Query Match 5.6%; Score 119.8; DB 4; Length 1959;
Best Local Similarity 55.0%; Pred. No. 1,5e-18;
Matches 294; Conservative 0; Mismatches 217; Indels 24; Gaps 2;

QY 561 AGATAATCAATCTTAAATACTGCTGACGTAATTAACAGTCCAGCAGCGGAGAGA 620
DB 411 AGATAACCGAATGATGCAAGATCAAGACATTAATCTTGAGCGCTATGCTTTAGA 470
QY 621 AGATTCACTTAACTTTAGCAGGCTCATTTACAGACAGAAAGCTGAATATATTAAT 680
DB 471 ACTTGACATTAACGCTGCTATACCGCTTTACAGAAATGCAAAATGAAAGATTCATTAT 530
QY 681 GCCTACGATATGCAAGCTGCAATGTGCAATTTATTAATTAAGGAGCGACGTTAAATA 740
DB 531 AATGTAATATGCTCAAGCTGCAATTTACACTTATTAATTAAGAGACGATCCCTTTT 590
QY 741 TAAAAAAGATGGGAGCTGCTGTCACCGCTGTATCCAGGCTCAGGAGAACTGATG 800
DB 591 TGGTAGTAATGGGGAGATGCAATCTTCGATTTACCA-----TA 632
QY 801 TAAAGAGCGGTAAAGCGAAATTAAGATTAATTAATTTAGTAGGTGATTA 860
DB 633 TTACCGAAGAAATGCAATGATATACAGAGAAATTTGACATTTGCTGCAATGATTA 692
QY 861 CAAGGTTTATGATCAATTAAGACAGCGGCTTACAGTCTGAAGTTGTCGAAATTA 920
DB 693 TACAGGCTTAAATTAATTAAGA-----GGAGCAAAATGCTGAAGTGTGGCGTATTA 746
QY 921 TAAATTCGTAAGAAATGACGTTGGCGGATTTGATTAATTTGATATTTCCACTTA 980
DB 747 TCAATTCGTAAGACCTTAAGGATTAATTAATTAATTAATTTCCCAAGCTA 806
QY 981 TGATTTGAAAAATATCAATTAAGCAACAGTGTAGATTAACTAGAGAAATTTATACAGA 1040
DB 807 TGATCTCGCACTTATTCATTAATGAGAGTGTGAGTTTACAGAGAAATTTATACAGA 866
QY 1041 TCCAGTGGGATATTCAGGGGAAATTAATGTTGGGAAACGTTTATGCTTAAAT 1095
DB 867 TCCAAATGGGAGAACAAAATGACCTTACAGGATTTGCAAGTGAATGTTTAAAT 921

RESULT 14
ADR89411
ID ADR89411 standard; cDNA; 1986 BP.
AC ADR89411;
XX
XX 18-NOV-2004 (first entry)
XX
XX AXMI-009 alternative start site coding sequence #2.
XX
XX ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX

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12/10/2019

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:00:54 ; Search time 5744.73 Seconds
(without alignments)
17469.639 Million cell updates/sec

Title: US-10-782-141-1

Perfect score: 2145

Sequence: 1 ttccaccaataatcattc.....atagttattcattcaatlaa 2145

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hic.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gsa1.*
10: gb_gsa2.*
11: gb_gsa3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	65.2	3.0	1101	10	CNS0039G
C 2	56.2	2.6	1101	10	CNS0182P
C 3	54.6	2.5	1225	10	CNS0161D
C 4	53.6	2.5	1101	10	CNS00001
C 5	53.4	2.5	1101	10	CNS0039G
C 6	53	2.5	1101	10	CNS0100X
C 7	51.8	2.4	1204	10	CNS016E2
C 8	50.6	2.4	928	10	CNS0102F
C 9	49.8	2.3	944	10	CNS002K1
C 10	49.6	2.3	1101	10	CNS00E5I
C 11	48.8	2.3	876	10	CNS009E1
C 12	48.4	2.3	938	10	CNS006TJ
C 13	48.2	2.2	1101	10	CNS0106X
C 14	48	2.2	663	3	BJ401008
C 15	47.2	2.2	1101	10	CNS001C0
C 16	46.6	2.2	867	11	CNS075B6
C 17	46.6	2.2	1146	10	CNS021G2
C 18	46.6	2.2	1193	1	AJ926097
C 19	46.4	2.2	443	3	BJ389293
C 20	46.4	2.2	572	3	BP256971
C 21	46.4	2.2	749	9	AZ903748
C 22	46.2	2.2	554	3	BJ432057

23	46	2.1	355	1	AA448366
24	46	2.1	511	6	CB158772
25	46	2.1	817	5	BU773209
26	46	2.1	1414	4	BC025177
27	46	2.1	7050	10	AY420513
28	45.8	2.1	456	3	BJ390240
C 29	45.8	2.1	764	9	BZ025901
C 30	45.8	2.1	1101	10	CNS003B6
C 31	45.8	2.1	1225	8	DN671106
C 32	45.8	2.1	1296	10	AG350007
C 33	45.6	2.1	698	9	BH940466
C 34	45.6	2.1	811	10	CZ534216
C 35	45.4	2.1	347	3	BJ399104
C 36	45.4	2.1	858	8	DR732187
C 37	45.4	2.1	982	10	CNS001T8
C 38	45.4	2.1	1101	10	CNS017X8
C 39	45.2	2.1	350	10	N97363
C 40	45.2	2.1	583	9	BH725336
C 41	45.2	2.1	1073	1	AJ928975
C 42	45.2	2.1	1099	10	CNS00DW8
C 43	45	2.1	572	11	CR332988
C 44	45	2.1	581	8	DN470449
C 45	45	2.1	581	8	DR755050

ALIGNMENTS

RESULT 1
LOCUS CNS0039G/c 1101 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL063921 GI:4941778
VERSION GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1101)

AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

COMMENT

- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutyo Oosawa and Aaron Mammose in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pi and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

1..1101
Location/Qualifiers
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/db_xref="taxon:7227"
/clone="BACR08K10"
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ORIGIN

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Db 762 RGRMGGRKRRRTARGGKDKTGKKKTKGDRDGGGGGDRGDGAGGGDRARARAR 821
QY 1053 TTCAGGGGGAATTAATGTTGGAGACGGTTTTTTTAACTTAATTCGGTAGAACAATG 1112
Db 822 WDTRDTRGADKADKKKAGKRRKTKTKRDTADKMAAMRWRRRKRDRRGR 881
QY 1113 AACACGGGACCTGTTTATGTAAGTTCAGGCTTAAAGATATATATAGTATTCTAT 1172
Db 882 WRWRGADKKMKDDDDTADKTDWTATAGATAGMDDKAKDGDWKRKGTDMRTWKRT 941
QY 1173 TAATCTTACGCTTGTATCTAGTGTGGGGGGGAGACCTGCATTATGAACATTCAC 1232
Db 942 WKMGRRGDKRGTAGRAGDGKKKKDKDRDADAADGKDTWBDTDTAKRRRRKR 1001
QY 1233 AAAGGTAAACGCTGCTTTTCAACGTATGCTGGA 1267
Db 1002 RRAGRRGRDKGDKKKRRARWRKGGKTKTKD 1036

RESULT 5
CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL063921 GI:4941778
VERSION AL063921
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
REFERENCE Direct Submission
AUTHORS Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
TITLE BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
JOURNAL - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoler in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
1. 1101
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ORIGIN
Query Match 2.5%; Score 53.4; DB 10; Length 1101;
Best Local Similarity 22.3%; Pred. No. 0.095;
Matches 102; Conservative 156; Mismatches 199; Indels 0; Gaps 0;
QY 1 TTTCACCAATATATATGTTTTTTGTAGAAACATTTTACAGAAATCATTTGGGTACTA 60

Db 411 TTTTAAABAAABAAATTAATTTAAABAAABAAATTTAAABAAABAAATTAATTTATWT 470
QY 61 CGAATATATAGAAAGACACCTGGCATATATTATTATAGTGTCTTAAATTAAGACATATA 120
Db 471 AAAAAAAAAAAATTTTTTTTTTTAAWTATATATTTTAAATAAAAAAAAAAAWA 530
QY 121 TAAGAGTGAATAAATATGAATCTTATGCAATTAACAATATGAATATGAATCTGATGGT 180
Db 531 AAAAAAAAAATTAATTTTAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATA 590
QY 181 TCCCGAATTAACAATAATATGCAACAGATATCTTTTGAACAAGATCCAAATATATTT 240
Db 591 TNNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHT 650
QY 241 CCTATTAACTGAGACGCTTGCAAGGAAGCCATGCAAGATACSTGGAAATCACTGCG 300
Db 651 YNNHNNHNNHNNHNNHNNHNNHNNHNNHNNHNNHNNHNNHNNHNNHNNHNNHNNHNN 710
QY 301 GATATATGATACATTTGGGACATACCTTATGCAATCTGTAGAACCGGTATAGTGA 360
Db 711 NHTHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTN 770
QY 361 ATTCCGTATATTTTCAATATTAACAACATCTCCGTTCTGTCATCTGTGCA 420
Db 771 HYAAAAAAMAATTTNNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHT 830
QY 421 GCACCTTCTATATGATGATTTAGTATCTATATCTGTA 457
Db 831 HMMWTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTNHTN 867

RESULT 6
CNS0100X 1101 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION BACN03G04 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL098379 GI:5609990
VERSION AL098379
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
REFERENCE Direct Submission
AUTHORS Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
TITLE BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
JOURNAL - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
<http://www.edgp.biol.ac.uk> - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billand at CERH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.
Location/Qualifiers
1. 1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN03G04"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : SP6"

ORIGIN
Query Match 2.5%; Score 53; DB 10; Length 1101;
Best Local Similarity 16.2%; Pred. No. 0.12;

Matches 102; Conservative 259; Mismatches 267; Indels 1; Gaps 1;

```

QY 704 ATGTCATTATTATTAAGGAGCAGTTAAATATAAGAAAGGAGGACTAGT 763
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 451 DMTDTKTTTWTWTWTWTGKMDTKTKTKMDDDGTTWTDKMDKTDKTDV 510
QY 764 GTCACCGGTGTATCCAGGCTCAGGAGAACTGATTGACAGCGGTAAAGCGAAA 823
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 511 WADNAGWTTDKTKYAKKKTDTKTKTKTKTKTKTKTKTKTKTKTKTKTK 570
QY 824 TAAAGAGTATTAATTAATGTTAGGCTGTATTAACAAGGTTTATGATCAGTAAGAC 883
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 571 ABADRAANAKDADGADDTATKTDGTTGTTKADTTDDADMDKMDKMDKADTKAG 630
QY 884 AGCGGCTACAGTGTGGAAGTTGTCGAATTTAAATTTGTAAGAAATGACGT 943
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 631 RKGWGWGKKGKGTTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTK 690
QY 944 TGGCGGTATGATATTTATGCTATATTTCACTTATGATTTGAAAAATATCATAG 1003
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 691 GGGDSTAKDRAVAMPAKATRAAAADATATAATKATATATTKTKTKTKTK 750
QY 1004 CAACAAGTATGATTAAGGAAATTTATACAGATCCAGTGGATTTAGGGGAA 1063
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 751 TTTTCTTTTCTTTAKADRDGDDAKRGGDDGDDMDKMDKMDKRDGDDTK 810
QY 1064 ATATGCTTGGGAAAGGCTTTTATGCTT-TAATTCGTAGAGAAATGAAACGGGGA 1122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 811 GKKKKAKKDKHKTMMWADDTGTAMATWAKTATKTKAKATKDBKRGGGGGRG 870
QY 1123 CTGCTTATGCTTCTGCTTCAAGCTATGATATATATGCTATTTATTTCTTACG 1182
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 871 GRRRARGRGRGRGRGRGRGRGRGRGRGRGRGRGRGRGRGRGRGRGRGR 930
QY 1183 CTGCTTATGCTTCTGCTTCTGCTTCAAGCTATGATTAAGGCTTCAACAAGGCTTAC 1242
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 931 TWKTWTGTTGTTTWTWKRRGRGRGRGRGRGRGRGRGRGRGRGRGRGR 990
QY 1243 GGTGCTTTTCAAGCTATGCTTCAAGCTATGATTAATTCATTTATTTTGGC 1302
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 991 DMKDKMKMTDGMGKGWGRGKAGADGAKRRGRGRGRGRGRGRGRGRGR 1050
QY 1303 AATACCATATATTTAAATTTATTTCAAT 1331
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1051 WADDMDADYDDADADYMKKATWMDW 1079

```

RESULT 7
CNS016E2/c 1204 bp DNA linear GSS 26-JUL-1999

LOCUS
DEFINITION
BACN15A12 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION
VERSION
SOURCE
KEYWORDS
ORGANISM
AL106628.1 GI:5622852
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS
TITLE
JOURNAL
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequenage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billand at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MC
project grant. The DNA was prepared from embryos by Alain Bucheton

and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES
source
1. 1204
/location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN15A12"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : T7"

ORIGIN

Query Match 2.4%; Score 51.8; DB 10; Length 1204;
Best Local Similarity 21.7%; Pred. No. 0.24;
Matches 98; Conservative 162; Mismatches 190; Indels 1; Gaps 1;

```

QY 576 TAAAAAATGCTGAGCTAGTTAAACAGTTCCAGACCGGAGAGATTTCATAACT 635
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1197 KAAAAAATATWAKWAKATATAKAWKAKAKWAAAAAATAAATAAATAA 1138
QY 636 TTAGACGGTCAATTAACAGACAGAAAGCTGAATATTATTGCTGATGTGCA 695
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1137 KAAAAAATAAADAADAADAADAADAADAADAADAADAADAADAADAADA 1078
QY 696 AGCTGCAATGTCATTATTATTAAGGACGAGTTAAATATATAA-AAGAATGGG 754
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1077 WKATGKDDDDKRAADAKKKKKKAAADKADKADKADKADKADKADKADK 1018
QY 755 GACTAGTGTCCACCGGTGTATCCAGGCTCAGGAGAACTGATTGTAACGACGGTTAA 814
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1017 KDKKKDDATDAWAAKAKKKDKKAKKKKKDKKAKKAAWKKDKDKKKKK 958
QY 815 AAGCGAAATGAAAGTATTAATTAATTTGTTAGGCTGTTAAACAAGGTTAGATC 874
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 957 KKKKKKKKAAKDDAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 898
QY 875 AGATAAGACAGCGGGTACAGTGTGAAGTTTGTGGAATTTAAATTTGTAAG 934
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 897 DKAAKKKAAKKKDDKKAADKKAADKKAADKKAADKKAADKKAADKKA 838
QY 935 AATGACGTTGGCGGTATGATATTTGCTATTTTCACTTATGATTTGAAAAAT 994
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 837 AAATGACGTTGGCGGTATGATATTTGCTATTTTCACTTATGATTTT 778
QY 995 ATCCATTAGCAACAGTATGATTAAGTAACTAG 1025
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 777 GAKWAKKTRAAADAKGADATTAATAAARAAG 747

```

RESULT 8
CNS0102F/c 928 bp DNA linear GSS 26-JUL-1999

LOCUS
DEFINITION
BACN03B09 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION
VERSION
SOURCE
KEYWORDS
ORGANISM
AL098433
AL098433.1 GI:5610044
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS
TITLE
JOURNAL
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequenage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC

melanogaster BAC library was prepared by Kazutoyo Oseegawa and Aaron Mammose in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPci-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

```
1. .1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR29L15"
/clone_1lb="RPci-98"
/notes="end : TET3"
```

ORIGIN

Query Match 2.3%; Score 49.6; DB 10; Length 1101;
Best Local Similarity 21.0%; Pred. No. 0.8;
Matches 112; Conservative 171; Mismatches 250; Indels 0; Gaps 0;

```

Qy 630 TAACTTTTACGAGGTCATATCAAGACGAAAGCTGAATATTATTGCTTACGTA 689
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1082 KRWMTAKATTAARAGAWGMRRTGADRWGMDGRTATRAWTADTTGGAGARAGK 1023
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 690 TGTGCAAGTCGCAATGCGATTATTAATTAAGGACGACGAGTGAATTAATAAAGA 749
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1022 GKDDTWAAGGTATATATGTTGGDMMWKKRTTATRAAKGTAKMGAKAGATRAWT 963
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 750 ATGGGAGCTAGTGTGTCACCGTTGATCCAGGTCGAGGAGAACTGATTTGAACGACG 809
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 962 AKDPAATKKDXMGATGDTTGTGMAAGRTTGWGTTDDMGKAGATKTTTGTGATGAG 903
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 810 GTTAAAGCGAAATTAAGATATCTAATATTGTTGAGGTTGATTAACAAGGTTT 869
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 902 AGAAGKAGWGWGMDAGTRWGMGRADTDKGMPTGKGTGDKGTTKRWAKTTT 843
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 870 AGATCAGATTAAGACGCGGGTCAAGTGCAGGTTGCGCAATTTAATTAATTTGCG 929
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 842 KTRTTATATATATATATATATATATATATATATATATATATATATATATATAT 783
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 930 TAGAGAAATGACGTTGCGGATTTGATATATATATATATATATATATATATAT 989
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 782 ADADKAGTAGWAGATATATATATATATATATATATATATATATATATATAT 723
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 990 AAAATATCCATTAGCAACAAGTGTAGATTACTAGGAAATTTATACAGATCCAGTGG 1049
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 722 RTWDKAARARAGWMAATRTGWAARADRWMAAATATATATATATATATATAT 663
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1050 ATATTCAGGGGAAATTAATGTTGGGAAAGGTTTATGCTTAATTCGATAGAGAA 1109
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 662 DTKTRATATGTTKTKAKATTTGDDTATTTDRKTTKGTGAGDGGWRDGGKRGTA 603
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1110 TGAACAACGGGACCTGTTTACTTCTGCTTCAAGCTATAGATATATATA 1162
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 602 AATRAARAVGKATKADWMDHTTTTWMKMTTKTKDRMTTGTGRTTTTWT 550
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 11
CNS009G1/c 876 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BACR19J14 of RPci-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL053529.1 GI:4935018
VERSION AL053529
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

REFERENCE

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 876)
Genoscope.
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oseegawa and Aaron Mammose in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPci-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

```
1. .876
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR19J14"
/clone_1lb="RPci-98"
/notes="end : TET3"
```

ORIGIN

Query Match 2.3%; Score 48.8; DB 10; Length 876;
Best Local Similarity 44.9%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 83; Conservative 18; Mismatches 84;

```

Qy 64 ATATATAGAAAGACACCTGCGATATATTTTATAGTGTCTTAAATTAAGACTATATA 123
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 798 ATATATATATATATATATATATATATATATATATATATATATATATATATAT 739
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 124 GAGTGAATAATATGAAATTTTATCAATAATACAAATGATATGAATTTGATGTTCC 183
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 738 ATATATATATATATATATATATATATATATATATATATATATATATATAT 679
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 184 CGAATTAACCAATATGCAACAGATATCCCTTTGCAAGAGATCCAAATATATTTCC 243
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 678 WAAATATATATATATATATATATATATATATATATATATATATATATATAT 619
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 244 ATTA 248
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 618 WTTTA 614
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 12
CNS006TV/c 938 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC #
DEFINITION BACR14J11 of RCT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL065906 GI:4944874
VERSION AL065906
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 938)
Genoscope.
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

DEFINITION Bf401008 Dictyostelium discoideum cDNA library, SF Dictyostelium
discoideum cDNA clone dds15e22 3', mRNA sequence.
ACCESSION Bf401008
VERSION Bf401008.1 GI:19333925
KEYWORDS Dictyostelium discoideum
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
REFERENCE Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
AUTHORS 1 (bases 1 to 663)
TITLE Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
JOURNAL Full length cDNA of Dictyostelium discoideum at the slug stage
COMMENT Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
source
1..663
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:4689"
/clone="dds15e22"
/sex="mat A"
/dev_stage="Slug stage"
/clone_lib="Dictyostelium discoideum cDNA library, SF"
ORIGIN
Query Match 2.2%; Score 48; DB 3; Length 663;
Best Local Similarity 56.2%; Pred. No. 1.8;
Matches 90; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 89 ATTATTAGGTGCTTAAATAATAGCACTATATAGAGCAAAATATGATCTATC 148
DB 362 AATATTAGGGGTAAAGATTAACACCTGCTGTAATCAAAATTTTCAACCTATG 303
QY 149 AAAATACAAATGATATGAATTTCTGATGCTCCGAAATACAAATATGTCAACA 208
DB 302 AATACATGAAGATTAATATATCTAGATATGCTGATACAAATGTTTATGCCCCAGT 243
QY 209 GATATCTCTTTGCAAGATCCAAATATATTTCTATTAA 248
DB 242 CAATTCATCTGAAATGATACAAACAGTTCCCTTAAA 203
RESULT 15
CNS00100/c 1101 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC.
DEFINITION BACR32D23 of RPECI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL068607
VERSION AL068607.1 GI:4958689
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage;
BP 101 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Oscegawa and
Aaron Mammober in Pictet de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPECI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
source
1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR32D23"
/clone_lib="RPECI-98"
/note="Tend : TET3"
ORIGIN
Query Match 2.2%; Score 47.2; DB 10; Length 1101;
Best Local Similarity 20.2%; Pred. No. 3.1; Indels 0; Gaps 0;
Matches 96; Conservative 158; Mismatches 221; Indels 0; Gaps 0;
QY 792 AACTGATTGTAACGAGCGTTAAAGCAAAATATAAGTATATTAATTGTGAGG 851
DB 897 WDWKDAWKGDKDKTKKKKKKKGKAKGRABAAAADRGAAADGDAKTKTKAKTKWK 836
QY 852 GTGTATTAACAGGTTTAATCAGATTAACAGCGGGGTGACAAAGTCTGAAGTTGTC 911
DB 837 KKKGGGWRGTRGKGGKGTTRAGDTKKKKKKKKGGDKKRTTKTKTKTGTTGT 778
QY 912 GAAATTAATAAATTTGTAAGAAATGACGTTGCGGTATGGAATATTAATGCTATAT 971
DB 777 AMTKTKGKKKKKKKKKKKKDKMTGKTGKTGKTGSGGKKTKTKGKTWMA 718
QY 972 TCCAATTAATGATTTGAAATAATATCCATTAGCAACAGGTGATTAACAGGAAT 1031
DB 717 AMRAKTKTKTKKKKGTAKTADTKKKKKKKDKGTTGKKMKGTGKAAMWGDTGTRDKK 658
QY 1032 TTATACAGATCCAGTGGGATATTCAGGGGAAATTAATGTTGGAAACGTTTATGCTT 1091
DB 657 KKAAAMWMDTTDKTKAKKADTAADTGKKKAKATKAARAKGAWPADADGDTKAKTGTXT 598
QY 1092 TAAATCGGTAGAACAAATGGAACACGCGGACCTGTTAGTACTTGCTCAAGCTAT 1151
DB 597 KADDTGKGAAGKAGKGRKRTDKGAKGDKATAGAKKKTAKKGDADKAGKGRADGG 538
QY 1152 AGATATATATATGTCATTTATATCTTCAGCTTGTTATTAAGTGGCGGGGAAC 1211
DB 537 ARTTRGKKKKAAGTKKDKKDKGTDKAGTTRGTGKBRAGKGDGADGDKGTGKGGAR 478
QY 1212 TCCTCATTAATGAAGACTTCAAGGTAACGCTGTTTCAACGATGCTGGA 1266
DB 477 GKAAAGVAGAAATGAGGAGAKRGGTGTRKAGGAGWGRDAGWGRAXGR 423
Search completed: December 19, 2005, 12:54:26
Job time : 5749.73 secs

11-11-11

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:00:43 ; Search time 7232.94 Seconds
(without alignments)
16857.498 Million cell updates/sec

Title: US-10-782-141-1

Perfect score: 2145
Sequence: 1 ttccaccaataatcatgtt.....atagttattatcaatcaa 2145

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5683141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmb1:*
1: gb_da:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sta:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2145	100.0	2145	6	CQ868324 Sequence
2	2019	94.1	2019	6	CQ868325 Sequence
3	2010	93.7	2010	6	CQ868327 Sequence
4	949.2	44.3	3746	1	AB074414 Bacillus
5	855	39.9	5980	6	CQ868311 Sequence
6	812.4	37.9	4100	1	AB112346 Bacillus
7	747.2	34.8	2082	6	CQ868312 Sequence
8	739.8	34.5	2073	6	CQ868314 Sequence
9	214	10.0	3931	1	AB161456 Bacillus
10	197.2	9.2	2028	1	BTU8189
11	180.6	8.4	2024	1	BTU8188
12	172.4	8.0	3468	6	AR143378 Sequence
13	172.4	8.0	3468	6	AR567184 Sequence
14	172.4	8.0	3471	6	BD062618 Toxins ac
15	172.4	8.0	3471	6	BD128371 Toxin act
16	172.4	8.0	3471	6	AR205863 Sequence
17	172.4	8.0	3471	6	AR339971 Sequence
18	172.4	8.0	3471	6	AR559861 Sequence

19	172.4	8.0	3726	6	AR143379 Sequence
20	172.4	8.0	3726	6	AR567185 Sequence
21	172.4	8.0	3837	1	BTCRYIGL
22	172.4	8.0	12579	1	BTCRYI
23	162.8	7.6	2407	6	AR359378 Sequence
24	162.8	7.6	2407	6	AR098659 Sequence
25	147.4	6.9	3668	1	AB185105 Bacillus
26	133.6	6.2	4391	1	BTJEG65
27	119.8	5.6	1959	6	AR359366 Sequence
28	119.8	5.6	1959	6	AX098635 Sequence
29	118.4	5.5	1986	6	CQ868322 Sequence
30	118.4	5.5	2016	6	CQ868320 Sequence
31	118.4	5.5	2049	6	CQ868318 Sequence
32	118.2	5.5	3696	1	AY138457 Bacillus
33	118.2	5.5	3842	1	BTMCRYIBC
34	118.2	5.5	3934	1	BACCRYE
35	118.2	5.5	3934	6	AR068828 Sequence
36	118.2	5.5	3934	6	I38760
37	118.2	5.5	3934	6	I70138
38	118.2	5.5	8306	1	BTU70726
39	117.6	5.5	1806	6	CQ868303 Sequence
40	117.6	5.5	1890	6	CQ868301 Sequence
41	117.6	5.5	2190	6	CQ868300 Sequence
42	116.8	5.4	2549	1	AY570734 Bacillus
43	116.8	5.4	3684	1	AF077326 Bacillus
44	116.8	5.4	3684	6	I90319
45	116.8	5.4	3684	6	AR359400 Sequence

ALIGNMENTS

RESULT 1	CQ868324	2145 bp	DNA	linear	PAT 13-SEP-2004
LOCUS	CQ868324	Sequence	25 from Patent WO2004074462.		
DEFINITION	CQ868324				
ACCESSION	CQ868324				
VERSION	CQ868324.1	GI:51998370			
KEYWORDS					
SOURCE					
ORGANISM	Bacillus thuringiensis				
	Bacillus thuringiensis				
	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus				
	cereus group.				
REFERENCE					
AUTHORS	Carozzi, N., Hargiss, T., Koziel, M.G., Duck, N.B. and Carr, B.				
TITLE	Delta-endotoxin genes and methods for their use				
JOURNAL	Patent: WO 2004074462-A 25 02-SEP-2004;				
	Athenix Corporation (US)				
FEATURES					
source	1. 2145				
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ORIGIN					
Query Match	100.0%	Score 2145;	DB 6;	Length 2145;	
Best Local Similarity	100.0%	Pred. No. 0;			
Matches 2145;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	TTTACCAATATATATGTTTGTGAGAAACATTGTAACAGAAATACATTGGGGTACTA	60		
DB	1	TTTACCAATATATATGTTTGTGAGAAACATTGTAACAGAAATACATTGGGGTACTA	60		
QY	61	CGAATATATAGAAAGACCTGGCATATATTTATTTGTTGTTTAAATTAAGACTATA	120		
DB	61	CGAATATATAGAAAGACCTGGCATATATTTATTTGTTTAAATTAAGACTATA	120		
QY	121	TAAAGAGTAAATATGAAATCTTATCAAAATACAAATGAAATGAAATTCGATGGT	180		
DB	121	TAAAGAGTAAATATGAAATCTTATCAAAATACAAATGAAATGAAATTCGATGGT	180		
QY	181	TCCCGAATACCAATATATGCAACAGATATCTTTGCAAGAGATCCAATATATTT	240		

Db 181 TCCCCGAATACAAATATGTCMAACAGATATCTTTTGCAAGATCCAAATATATTT 240
QY 241 CCTATTAACTGGAGCTTGTCAGGGAAGGCCATGCGAAGATGCTGGAAATAGCTCG 300
Db 241 CCTATTAACTGGAGCTTGTCAGGGAAGGCCATGCGAAGATGCTGGAAATAGCTCG 300
QY 301 GATATAGTAACTATTGGGACATACCTTATCAATTCCTTGCTAGAACCCGGTATAGGTGA 360
Db 301 GATATAGTAACTATTGGGACATACCTTATCAATTCCTTGCTAGAACCCGGTATAGGTGA 360
QY 361 ATTCTGTAATATTTCATATTAATTAACAAATCATCTCCGCTCTTGCTGATCTGTGGCA 420
Db 361 ATTCTGTAATATTTCATATTAATTAACAAATCATCTCCGCTCTTGCTGATCTGTGGCA 420
QY 421 GCACCTTATATATGATTTAGTATCTATATTCGTAAAGAGTAAAGGATGACGACCGGTGA 480
Db 421 GCACCTTATATATGATTTAGTATCTATATTCGTAAAGAGTAAAGGATGACGACCGGTGA 480
QY 481 AGTACGGGGTTCAGATTTTGGAGGTGAATGATGCTGTATCAAGATTTATCTTCAT 540
Db 481 AGTACGGGGTTCAGATTTTGGAGGTGAATGATGCTGTATCAAGATTTATCTTCAT 540
QY 541 TATCTTGAAGATGGCTTACAGATTAATCAATCTTAAATCTTGCTGACGTAGTTAAA 600
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QY 601 CAGTTCACAGCAGGGGAGAAATTCACATACTTTAGCAGGGTCAATTAATAAGACG 660
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Db 661 AAAGCTGAATATTAATTTATTCCTACGTATGCAAGCTGCAAAATGTCATTTATTTACTA 720
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Db 721 TTAAGGACCCAGTTAAATTAATAAAGAAATGGGACCTAGTGTGTCACCGTGTATCCA 780
QY 781 GGGTCAAGGAGACCTGATTCGTAACGAGCGGTTAAAGCCGAAATTAAGAGTATCTAAT 840
Db 781 GGGTCAAGGAGACCTGATTCGTAACGAGCGGTTAAAGCCGAAATTAAGAGTATCTAAT 840
QY 841 TATGTGTAGGGTGTATTAACAAGGCTTTAGATCAGATAAGACGCGGGTCAAGAGTCT 900
Db 841 TATGTGTAGGGTGTATTAACAAGGCTTTAGATCAGATAAGACGCGGGTCAAGAGTCT 900
QY 901 GAAGTTTGTGCAAAATTAATTAATTTGTAAGAAATGACGTTGGCGGTATTTGATATTT 960
Db 901 GAAGTTTGTGCAAAATTAATTAATTTGTAAGAAATGACGTTGGCGGTATTTGATATTT 960
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Db 1021 ACTAGGGAATTTATACAGATCCAGTGGATTTTCAAGGGGAAATTTTGTGTGGAAACGG 1080
QY 1081 TTTTATAGCTTTTAATTCGTAGAAACAAATGAAACACGGGACCTGTGTTTATGTTACTGG 1140
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Db 1201 TGGGGGGGAACTGCTCATTAATGAAGACCTTCAAAAGGGTAAAGGTTGCTTTTCAACGTATG 1260
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Db 1381 CTTGTTTCACTGCAAGAAATTTTTCGCAACAACATAATCTTCTGTATAGGTAAAC 1440
QY 1441 AGTTCTGGGTACTCAGACAAATTTGAATCTGTGTTTACAGAGTATTAATTAAGATCTACCA 1500
Db 1441 AGTTCTGGGTACTCAGACAAATTTGAATCTGTGTTTACAGAGTATTAATTAAGATCTACCA 1500
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Db 1501 CCTAGTCGTAACAAATTAATCTCTATGATTAATCAAAATGGGACATGTTCAAAATGAACC 1560
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Db 1741 CCTTATCAAGCAAGTTTAAATTAATTAATTAATCTTCTGCAACCCAGCAATTAATTAACGCT 1800
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Db 1801 GTTAACTTCGCTAGAGCGAGTGAAGACCTGGTCCGTTCCAGTGAAGAGATGTCGCCA 1860
QY 1861 AGTTCTGTTTCAAAATGCTAATTTTCTGTCCAGCTACAGGAGGCTATATGTTCAATTTGAT 1920
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Db 1921 TATGTGACACCTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1980
QY 1981 CTATCTGTTACCACTTATTTGTTGACAAAGTCAATTTATCCAAATGACATCCAAATTT 2040
Db 1981 CTATCTGTTACCACTTATTTGTTGACAAAGTCAATTTATCCAAATGACATCCAAATTT 2040
QY 2041 GAAAAATGTAAGAAATGCAATTTGCAAGGAGACATATGTAATGTAAGAGATGTAACATCC 2100
Db 2041 GAAAAATGTAAGAAATGCAATTTGCAAGGAGACATATGTAATGTAAGAGATGTAACATCC 2100
QY 2101 TTGGAACACAAAAAGAGATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2145
Db 2101 TTGGAACACAAAAAGAGATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2145

RESULT 2
CO868325 2019 bp DNA linear PAT 13-SEP-2004
LOCUS CO868325
DEFINITION Sequence 26 from Patent WO2004074462.
ACCESSION CO868325
VERSION CO868325.1 GI:51998371
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE
1 Carozzi,N., Hargiss,T., Koziel,M.G., Duck,N.B. and Carr,B.
AUTHORS Delta-endotoxin genes and methods for their use
TITLE Patent: WO 2004074462-A 26 02-SEP-2004;
JOURNAL

FEATURES
Source

Athenix Corporation (US)

Location/Qualifiers

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/mol_type="unassigned DNA"

/db_xref="taxon:1428"

CDS

1..2019

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ORIGIN

Query Match 94.1%; Score 2019; DB 6; Length 2019;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 127 GTGAAAATATGATCTTATCAAAATCAAAATGATGAAATTCGATGCTCCCG 186
Db 1 GTGAAAATATGATCTTATCAAAATCAAAATGATGAAATTCGATGCTCCCG 60

Qy 187 AATAACACAATATGTCMAACAGATATCTTTGCAAGATCCAAATATATTTCTATT 246
Db 61 AATAACACAATATGTCMAACAGATATCTTTGCAAGATCCAAATATATTTCTATT 120

Qy 247 AACCTGACGCTTGTCCAGGAAGCCATGCGAAGATACGTGGGAATCAGTCTCGGATATA 306
Db 121 AACCTGACGCTTGTCCAGGAAGCCATGCGAAGATACGTGGGAATCAGTCTCGGATATA 180

Qy 307 GTAATCTATGGAATCATCTTATCAATCTTGTCTAATACCCGGTATAGGTGGAATTCCT 366
Db 181 GTAATCTATGGAATCATCTTATCAATCTTGTCTAATACCCGGTATAGGTGGAATTCCT 240

Qy 367 GTAATATTTCAATATATAACAACATCATTCGGTCTTCTGTCATCTGTGGCAGCACTT 426
Db 241 GTAATATTTCAATATATAACAACATCATTCGGTCTTCTGTCATCTGTGGCAGCACTT 300

Qy 427 TCTATATGATATTTAGTATCTATTAATTCGTAAGAGGTAGACGAGAGCGTATTAAGTAC 486
Db 301 TCTATATGATATTTAGTATCTATTAATTCGTAAGAGGTAGACGAGAGCGTATTAAGTAC 360

Qy 487 GGGGTGCAATATTTGAGGTGAAATGATCGCTTATCAAGATTATATCTTCAATATCTT 546
Db 361 GGGGTGCAATATTTGAGGTGAAATGATCGCTTATCAAGATTATATCTTCAATATCTT 420

Qy 547 GAGGATGGCTTACAGATAATCAATCTTAATAAACTTGCTGACGATGTTAAACAGTTC 606
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Db 481 CAAGCAGGGAAGAAATTTCACTAACTTTAGCAGAGGTCAATTATCAGACAGAAAGCT 540

Qy 667 GAAATATTTATTTGCTACGATATGTCAGACGTCGAATGTGATTTATCTATTAAG 726
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Qy 847 GTAAGGATGATATAACAAGGTTTATGATCAATATAGACAGGCGGGTACAGTGTGAAAGTT 906
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Qy 907 TGGTCGAAATTTATATAATTTCTGAGAAATGACGTTGGCGGATATGATATTTATTTCT 966
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Qy 967 ATATTTTCAACTTATGATTTTGAATAATTCCTATAGCAACAAGTGTAGTTACTAGG 1026
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Qy 1087 AGCTTTAATTCGGGTAGACGAATGGAACAACGGGGACCTGTTAGTTACTTGGCTTCAA 1146
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Qy 1147 GCTATAGATATATATATGATCTATCTTATCTTCACTTGTGCTGCGGGG 1206
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Qy 1507 CGTACAAATTAATCTCTATAGATTTCAATGCGGCATGTGTTCAAAATGAACCTTCAGA 1566
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Qy 1627 AAAATTAACGCAATTTCTGCAATGAAAGCTTTTGCCCTACACAGAGTACAGATATGCA 1686
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Qy 1687 GAGGTTACGTCACAGCTGGGCTGTATATACAGAGAGATGTAGTAACGTTACCTTAT 1746
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Qy 1747 CAAGCAAGTTTAAATAATGCTTTAATCTTGTGACCCACGAAATTAATTAACGTTTGA 1806
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Qy 1807 CTTGCTACGCGAGTGAAGACCTGCTGCTTCCGATGTAAGAAAGATGTGCGCAAGTCT 1866
Db 1681 CTTGCTACGCGAGTGAAGACCTGCTGCTTCCGATGTAAGAAAGATGTGCGCAAGTCT 1740
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QY	1336	GAATTTTTCCGACAACTAAATACCTTCTCGTATGAGGTAAACAGTTCTGGGTACTCA <td>1455S</td>	1455S
Db	1201	AGATATGCAATGCAACCGTTGTTGGGATTCAAATCCACGGCATCTTGTTCAAGTCA <td>1266S</td>	1266S
QY	1396	GAATTTTTCCGACAACTAAATACCTTCTCGTATGAGGTAAACAGTTCTGGGTACTCA <td>1455S</td>	1455S
Db	1261	GAATTTTTCCGACAACTAAATACCTTCTCGTATGAGGTAAACAGTTCTGGGTACTCA <td>1320S</td>	1320S
QY	1456	CAGACAATTGAATCTGTGTTCACAGGTATTAATAAGATCTACACCTAGTGTCAAAAT <td>1515S</td>	1515S
Db	1321	CAGACAATTGAATCTGTGTTCACAGGTATTAATAAGATCTACACCTAGTGTCAAAAT <td>1380S</td>	1380S
QY	1516	TACTCTCATAGATTATCAAAATGCCGACATGTGTCAAAATGAAACCTCCAGAGTTAAAGTA <td>1575S</td>	1575S
Db	1381	TACTCTCATAGATTATCAAAATGCCGACATGTGTCAAAATGAAACCTCCAGAGTTAAAGTA <td>1440S</td>	1440S
QY	1576	TTTGCGTTGAGACATACAAAGTATGAAAAAGATAATCGAATTTATCCAGATTAATAATACG <td>1639S</td>	1639S
Db	1441	TTTGCGTTGAGACATACAAAGTATGAAAAAGATAATCGAATTTATCCAGATTAATAATACG <td>1500S</td>	1500S
QY	1636	CAAAATCTCTGACGTAAAAAGCTTTTGCCCTACACAGCAGGTACAGAGTATGACAGAGTTAC <td>1699S</td>	1699S
Db	1501	CAAAATCTCTGACGTAAAAAGCTTTTGCCCTACACAGCAGGTACAGAGTATGACAGAGTTAC <td>1566S</td>	1566S
QY	1656	GTCACAGCTGGGCGCTGTATACAGAGAGAGATGTATGATACGTTACCTTATCAAGCAAGT <td>1755S</td>	1755S
Db	1561	GTCACAGCTGGGCGCTGTATACAGAGAGAGATGTATGATACGTTACCTTATCAAGCAAGT <td>1620S</td>	1620S
QY	1756	TTAAATAATACGTTTAACTTCGACCCACGAAATTAATAATTCACCGTTAGACTTCGCTAC <td>1815S</td>	1815S
Db	1621	TTAAATAATACGTTTAACTTCGACCCACGAAATTAATAATTCACCGTTAGACTTCGCTAC <td>1680S</td>	1680S
QY	1816	GCGAGTGAGAGACCTGTCGTCGCTCCGATAGAAAAGATGTCGCAAGTCTGTTTCAAT <td>1875S</td>	1875S
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QY	1936	GTTACTCATTTATTCATCATGACGTGTGAATTAATTATACAAATCTATCTGTGTTACAC <td>1995S</td>	1995S
Db	1801	GTTACTCATTTATTCATCATGACGTGTGAATTAATTATACAAATCTATCTGTGTTACAC <td>1860S</td>	1860S
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Db	1861	CTTATTTGTTGCAAAAGTGAATTTATCCCAATTTGACATCCAAATTTGAAAAATGTACGAAA <td>1920S</td>	1920S
QY	2056	TGTCAATTCGAGAGACATATGTATGTGAAGAGATGACATCTTGGAACAACAAAAA <td>2115S</td>	2115S
Db	1921	TGTCAATTCGAGAGACATATGTATGTGAAGAGATGACATCTTGGAACAACAAAAA <td>1980S</td>	1980S
QY	2116	GAGATTTGTAATAGTTTATTTATCAATTAA <td>2145S</td>	2145S
Db	1981	GAGATTTGTAATAGTTTATTTATCAATTAA <td>2010S</td>	2010S
RESULT 4			
AB074414			
LOCUS	3746 bp	DNA	linear
DEFINITION	Bacillus thuringiensis serovar aizawai cry40A and 40orf2 genes for putative mosquitocidal toxin and Cry40ORF2 protein, partial and complete cds.		
ACCESSION	AB074414		
VERSION	AB074414.1	GI:16945771	
KEYWORDS			
SOURCE			
ORGANISM	Bacillus thuringiensis serovar aizawai		
	Bacillus thuringiensis serovar aizawai		
	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.		
REFERENCE	1		
AUTHORS	Ito,T., Sahara,K., Asano,S. and Bando,H.		
TITLE	Cloning and Expression of Novel Crystal Protein Genes from Bacillus		

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

thuringiensis subsp. aizawai Encoding a Mosquitocidal Proteins
Unpublished
2 (bases 1 to 3746)
Ito, T., Sahara, K., Asano, S. and Bando, H.
Direct Submission
Submitted (14-NOV-2001) Takekhi Ito, Graduate school of
Agriculture, Hokkaido University, Kita-9Jyou Nishi-9chome,
Kita-Ku, Sapporo-shi, Hokkaido 060-8589, Japan
(E-mail: ito-t@ads.agr.hokudai.ac.jp, Tel: 81-011-716-2487)

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AUTHORS Ito, T., Sahara, K., Asano, S. and Bando, H.
TITLE Cloning and Expression of Novel Crystal Protein Genes from *Bacillus thuringiensis* subsp. *aizawai* Encoding Mosquitocidal Proteins
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4100)
AUTHORS Ito, T., Sahara, K., Asano, S. and Bando, H.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2003) Takeshi Ito, Graduate School of Agriculture, Hokkaido University, Department of Applied Bioscience, Kita-9jo, Nishi-9chome, Kita-ku, Sapporo, Hokkaido 060-8589, Japan (E-mail: ito-t@obs.agr.hokudai.ac.jp, Tel: 81-11-706-2487 (ex.2487))
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DEFINITION Sequence 15 from Patent WO2004074462.
ACCESSION CQ868314

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VERSION CQ868314.1 GI:51998360
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REFERENCE
AUTHORS Carozzi, N., Hargiles, T., Koziele, M.G., Duck, N.B. and Carr, B.
TITLE    Delta-endotoxin genes and methods for their use
JOURNAL  Patent: WO 2004074462-A 15 02-SEP-2004;
        Athenix Corporation (US)
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 AB161456 3931 bp DNA linear BCT 03-FEB-2004
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ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 1
 Ikeya, T., Yamaya, K., Ito, T., Sahara, K., Bando, H. and Asano, S.
 Cloning and Expression of Novel Crystal Protein Genes from *Bacillus thuringiensis* subsp. entomocidus INA288
 Unpublished
 2 (bases 1 to 3931)
 Tomonori, I., Kumiko, Y., Takeshi, I., Ken, S., Shin-ichiro, A. and Hisanori, B.
 Direct Submission
 Submitted (30-JAN-2004) Ikeya Tomonori, Graduate School of Agriculture, Hokkaido University, Department of Applied Bioscience, Kita-9jo, Nishi-9chome, Kita-ku, Sapporo, Hokkaido 0608589, Japan
 (E-mail: ikeyana@s.agr.hokudai.ac.jp, Tel: 81-011-706-2487 (ex.2487), Fax: 81-011-706-2487)

TITLE
 JOURNAL

REFERENCE
 1
 Ikeya, T., Yamaya, K., Ito, T., Sahara, K., Bando, H. and Asano, S.
 Cloning and Expression of Novel Crystal Protein Genes from *Bacillus thuringiensis* subsp. entomocidus INA288
 Unpublished
 2 (bases 1 to 3931)
 Tomonori, I., Kumiko, Y., Takeshi, I., Ken, S., Shin-ichiro, A. and Hisanori, B.
 Direct Submission
 Submitted (30-JAN-2004) Ikeya Tomonori, Graduate School of Agriculture, Hokkaido University, Department of Applied Bioscience, Kita-9jo, Nishi-9chome, Kita-ku, Sapporo, Hokkaido 0608589, Japan
 (E-mail: ikeyana@s.agr.hokudai.ac.jp, Tel: 81-011-706-2487 (ex.2487), Fax: 81-011-706-2487)

FEATURES
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 Location/Qualifiers
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CDS
 1581
 1482
 1641
 1542
 1701

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ORIGIN

Query Match 10.0%; Score 214; DB 1; Length 3931;

Best Local Similarity 69.0%; Pred. No. 7.1e-30;

Matches 330; Conservative 0; Mismatches 130; Indels 18; Gaps 2;

QY 1564 AGAGTTAAGCTATTTGGTTGGACACATACAGATATGAAAAAGATATGCAATTTATCCA 1623
DB 1594 ACACCTCAGATGCTGTGGACACATGTAAGCGGATCCGTATATATGATTCACCA 1653
QY 1624 GATTAATTAACGCAAAATTCCTGCAGTAAAGCTTTTCCCTACAGCAGGTACAGATAT 1683
DB 1654 GATTAATTAACGCAAAATTCCTGCGGTGAAGCCTTTATATGGAATAC-----T 1704
QY 1684 GCAGAGGTTACGTACAGCTGGGCTGTATTACAGAGAGATGTATACCTTACT 1743
DB 1705 GGGGAAGGTCAAGTCTCTCTGCACTGTATTACAGAGCGATTTAGTAAAGTTACT 1764
QY 1744 TATCAAGCAAGTTAAATAATACGTTTACTTGCACCCGAGATATAAATTCAGTGT 1803
DB 1765 TATTAAGCAGTTTGAATAATACGTTTAAACCTTACATCCAGAGTAAATAATCCGTT 1824
QY 1804 AGACTTCGCTACGCGAGTGAGAGACCTGTCCGTTCCGATAGAAAAGATGTCGCCAAGT 1863
DB 1825 AGAGTTGCGTATGCAAGTATGAGAGCTGTACATTAACAGACAAAATGTGCGCGTAT 1884
QY 1864 TCTGTTCAATGCTAATTTTCTCGTCACTACAGGTGCTATAGTTCAATTTGAT--- 1920
DB 1885 GGTAGGTATTTCTAATTTTGGTATGATATACGGGTGATTCGATTAATTTAATAT 1944
QY 1921 -----TATGTGACACCTTATGTTACTACATTTAATCAATCAGTGTGTAATTTAT 1974
DB 1945 TTTAAATATTTAGAACTTTATCTGAATCAATTTAATATATCTGTTGTAATAATTA 2004
QY 1975 CAATATCTATCTGTTACACACTTATTTGTTGACAAAGTCAATTTATCCCAATTGACA 2032
DB 2005 CAATACTATCTTCTTCCGAACCTTATGTTGACAACTTGATTTATACCAATTTAA 2062

RESULT 10
BTU88189 2028 bp DNA linear BCT 01-OCT-1998
LOCUS Bacillus thuringiensis jegathesan insecticidal protein Jegt74 gene,
DEFINITION complete cds.
ACCESSION U88189.1 GI:3668334
VERSION U88189.1
KEYWORDS
SOURCE Bacillus thuringiensis serovar jegathesan
ORGANISM Bacillus thuringiensis serovar jegathesan
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
1 (bases 1 to 2028)
Kawalek,M.D. and Gill,S.S.
Isolation and characterization of insecticidal genes from Bacillus
thuringiensis subsp. jegathesan
Unpublished
2 (bases 1 to 2028)
Kawalek,M.D. and Gill,S.S.
Direct Submission
Submitted (29-JAN-1997) Entomology, University of California, 5419
Boyce Hall, Riverside, CA 92521, USA
LOCATION/Qualifiers
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/organism="Bacillus thuringiensis serovar jegathesan"
/mol_type="genomic DNA"

/sub_species="jegathesan"
/db_xref="taxon:56955"
1. .2028
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CDS

ORIGIN
Query Match 9.2%; Score 197.2; DB 1; Length 2028;
Best Local Similarity 54.6%; Pred. No. 1.2e-26;
Matches 524; Conservative 0; Mismatches 398; Indels 38; Gaps 5;

QY 136 ATGAATTCCTTATCAAAATACAAATGATATGAAATTCGTGATGTTCCCGCAATAACACA 195
DB 1 ATGAATTCCTTATCAAAATGAAATGTAATGTAATTTAAATGCTTCATGTAATTAACATA 60
QY 196 AATATGTCMAACAGATATCCTTTTCCMAAGATCCAAAT-----ATAATTTCC 242
DB 61 AATATGCCAAGATACATCCCTTTGCGAATGATTCAAATGCTGTGATGAAAAATGGAGAT 120
QY 243 TATTAACCTGACGCTGTGACAGGAAGCCATGACAGATACGTGGAAATCACTCCGGA 302
DB 121 TATTAAGATGTTGAATGAATGATGATGATTAATCTCTTCTATTTTGGAACACCTTGA 180
QY 303 TATTAAGATGTTGGACATACCTTATCAATTCCTTCTGTAAGAACCCGGATATGGTGAT 362
DB 181 GTTCTAGCAAGTATTTGTAATTTCTACTATTAATCTTGACAGATCTTCCATPAGAGAC 240
QY 363 TCCGTATATTTTCAATATTAACAACAATCTACCTCCGTTCTGTGATCATCTGTGGACG 422
DB 241 GCATTTGCTTATGTAAGTTCTATTTGAGAGATTTGGCCGAGACAGAAAGCTGTTCC-C 299
QY 423 ACTTCTATATGTGATTTAGTATCTAATATTCGTAAAGGTAGACAGAGCGTGTAAAG 482
DB 300 TTTGTCGTAGCGGAGATGTAATCGTTAATTCGTGAAGCGCTTGACCAAAACGTAATAA 359
QY 483 TGACGGGTTGACAGATTTTGAAGGTGAATGACCTGTTATCAAGATTTATATCTTCATTA 542
DB 360 CAGGGCAACGGGAAATTTTAACGGTTTAATGACATATTAACGGTATTAATTA 419
QY 543 TCTTGAGATTTGGCTTACAGATTAATCAATCTTAAAAAACTTGCTGA-----CGTAG 595
DB 420 TCTCCAAAGTTGTATGATACCTCGAATTCCTCGAATTCCTCAGGGGATTTGCAAGTTAG 479
QY 596 TTAACAGTTTCAAGCAG-----GGAAGAGATTTCACTAACTTTAGCAGG 644
DB 480 AGAAGCAGCTAGAAAGAGCTTGAAGAGATGAAGAGGATTTTGAAGAAAGCACTAGCAG 539
QY 645 GTCATTTATCAAGACAGAAAGCTGAATATTTATTTGCTACGTATGTGCAAGCTGCAAA 704
DB 540 TGAATTTGCAAGAGCGGTAGTCAATATGATTTATTAATCTATTTTGAACAAGCTGCAAA 599
QY 705 TGTGATTTATTTACTATTAAAGGACGCAAGTTAAATTAATAAAGATGGGACTAGTGTG 764
DB 600 TATTCATTTATCGATATTAAAGAGCTATGCAATTTAGAACAGATTTGGGTTAATAG 659
QY 765 TCCACCGTTGATTCAGGGTCAAGGAACTGA-----TTGTAAACGACGGTTAAAGC 818
DB 660 ACCTGAGGTGATACCTATTACTATGATGCGAAGATCTTTTGAAGAGCAATTTTATAT 719

QY 819 GAAATTAAGAGTACTAATTTTGTGAGGGTGTATACAAAGGTTAGATCAT 878
DB 720 GCGTATATAAAATTAATCTGATTCATTTGATTAATGATGATGATGATGATGAT 779
QY 879 AAGACAGGCGGGTCAAGTGTGAGTGTGCGAAATTTAATTAATTTGCTAGAGAA 938
DB 780 ACGTTACAGAGTTCAAGTGTGAGTGTGCGAGAGTTTAAATTTTCTAGAGAGAT 839
QY 939 GACGTTGCGGTATGATTAATTTGCTATATTTTCAACTTATGATTTTGAATAATTC 998
DB 840 GACATTAACGGTATTAATCTTGTGCTATATATCAACTATATTAATTAATTAATTC 899
QY 999 ATTGCAACAAGTGTAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1058
DB 900 AATACCAACCAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 959

RESULT 11
BTU8188
LOCUS 2024 bp DNA linear BCT 01-OCT-1998
DEFINITION Bacillus thuringiensis jegathesan insecticidal protein Jeg72 gene,
partial cds.
ACCESSION U8188
VERSION U8188.1 GI:3668332
KEYWORDS
SOURCE
ORGANISM
Bacillus thuringiensis serovar jegathesan
Bacillus thuringiensis serovar jegathesan
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
1 (bases 1 to 2024)
Kawalek,M.D. and Gill,S.S.
Isolation and characterization of insecticidal genes from Bacillus
thuringiensis subsp. jegathesan
Unpublished
2 (bases 1 to 2024)
Kawalek,M.D. and Gill,S.S.
Direct Submission
Submitted (29-JAN-1997) Entomology, University of California, 5419
Boyce Hall, Riverside, CA 92521, USA
LOCATION/Qualifiers
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ORIGIN
Query Match 8.4%; Score 180.6; DB 1; Length 2024;
Best Local Similarity 53.6%; Pred. No. 1.4e-23;
Matches 499; Conservative 0; Mismatches 384; Indels 48; Gaps 4;
QY 137 TGAATTTCTTATCAAAATATGATATGATTTGATGATGTTCCCGGATACCA 196
DB 2 TGAACCAATTCAGAAATTAATTAATTAATTAATTTGATGATTTTCAAGAAATACATGA 61

QY 197 ATATGCAAAAGATATCTTTTGGCAAGGATCCAAATATTTCTATTAA----- 248
DB 62 ATATGCCAAACAGATATCTTTTGGCAGATATCGAATGCTGTGATGATAAAAAATGGAA 121
QY 249 -----CTTGACGCTTGTGAGGGAAGCCATGGCAAGATACGTGGGAATCATGCTCGGA 302
DB 122 ATAAAGATTTGGGTAATGAATGTGAAGAGGATATATTTCTCTTCTCTGACAGACGA 181
QY 303 TATAGTACTATTGGGACATACCTTATACAAATCTTGCTGAAGCCGGTATAGTGAAT 362
DB 182 TAACTCAAGATAGTATGATTTGATTTGAAGAACTTGCTGAAGCTGTGACATCTTCTC 241
QY 363 TCTGTAAATATTTTCAATTAATAAC-----AACTCATTCGCTTGTGCTCAATCTGTG 418
DB 242 TGGCGGACTCAATTAATAAGCTCATTTGGGATTAAGTAAAGATTAAGATTAAGATTAAT 301
QY 419 CAGACCTTTCTATATGATTTTATGATCTATATTTGTAAGAGGTAGACGAGCTGT 478
DB 302 CGCAAGTTCTATGTGTCAGATCATCAATTAATTAATTAAGAGATTCAGAGCGATAC 361
QY 479 TAAGTGACGGGGTTCAGATTTTGAAGGTAAGTGAATGCTGCTTATCAAGATTTATCTTC 538
DB 362 TTGATTTGGGGAGTGTCTCACTTAATGCTCTTGCTATTTATTAATGAGATTAATCTGG 421
QY 539 ATTATCTTGAGATTTGCTTACAGATTAATCAATCCTTAATAAACTTGCTGACGTAGTTA 598
DB 422 GCGCTCGAGAGCTTGAATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 481
QY 599 AACAGTTCCAGACGAGGAAGAAAGATTTCTAATCACTTTTGAAGGCTCATTAACAAAC 658
DB 482 AGCGGTTTAAAGCTGTGAAGAAAGAAATTTTTCACAAAGCTTAATTAATTAAGAACTT 541
QY 659 AGAAGCTGAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 718
DB 542 CAGCTCGAGATTAAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 601
QY 719 TATTAAGGAGCAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 778
DB 602 TGTTAAGGAGATGCTGTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 651
QY 779 CAGGTCAGGAGAACTGATTTGAACGAGCGGTTAAAGCGAAATTAAGATTAATTAAT 838
DB 652 -----ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 697
QY 839 ATTATTTGTAGGAGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 898
DB 698 ATTAATGTTGATGAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 751
QY 899 CTGAAGTTTGTGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 958
DB 752 CTATAGATTTGGCTTGATTTAATTTCTTTTGTGAGATTAATTAATTAATTAATTAATTAAT 811
QY 959 TTAATGCTATATTTTCAACTTATGATTTTGAAGAAATTAATTAATTAATTAATTAATTAAT 1018
DB 812 TAGTTGCGATATTCACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 871
QY 1019 TAACTGAGGAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1049
DB 872 TCTTGTAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 902

RESULT 12
AR143378
LOCUS 3468 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 9 from patent US 6204246.
ACCESSION AR143378
VERSION AR143378.1 GI:15104664
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 3468)

Db 863 TTACTAATTAACCAATAGAAACAGATTTCAGTGTAGAGGTCATTATACAGATCCA 922

QY 1046 TGGGATATTCAGGGGAAATTATGTTGGGAA 1077

Db 923 TTGGTTTGTACATCGTAGTAGTCTTAGGGGA 954

RESULT 14

BD062618 3471 bp DNA linear PAT 27-AUG-2002

LOCUS BD062618

DEFINITION Toxins active against pests.

ACCESSION BD062618.1 GI:22608221

VERSION JP 2001507208-A/42.

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 3471)

AUTHORS Schnepf, E.H., Wicker, C., Narva, K.E., Walz, M. and Stockhoff, B.A.

TITLE Toxins active against pests

JOURNAL Patent: JP 2001507208-A 42 05-JUN-2001;

MYCOGEN CORP

COMMENT PN JP 2001507208-A/42

PD 05-JUN-2001

PF 01-JUL-1997 JP 1998504483

PI ERNEST H SCHNEPF, CAROL WICKER, KENNETH E NARVA, MICHELE WALZ, PI BRIAN A STOCKHOF

PC C12N15/32, C12N15/68, C07K14/325, A01N63/00, A01H5/00 CC

Strandedness: Single;

CC Topology: Linear;

FF Key Location/Qualifiers.

FEATURES

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Query Match 8.0%; Score 172.4; DB 6; Length 3471;

Best Local Similarity 54.2%; Pred. No. 4.2e-22;

Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 287 GGGATCAGTCTCGATATAGTAACTATTTGGGACATCTTATCAATTCCTTGCTAGAAC 346

Db 158 GCATGACGAGAAAGAGCATATCTATTTGGGACACCATATGCTCTTATACACAC 217

QY 347 CCGGTATAGGTGGAATTCCTGTAAATTTT-----CAATTAATAACAACTCATTCGGT 400

Db 218 CTCTCTTACTGCGATTTATTTCAATAGTATGTACCTTAATAGTAACTAGAGAGTA 277

QY 401 CTCTGTCATCTGTGGGACGACCTTCTTATATGTATAGTATCTATATTCGTAAG 460

Db 278 GTAGTGAACATATCATATCGAATTTGCTATATGTAGCTATATTTATTTATTTAC 337

QY 461 AGGTAGACGAGCGGTATAGTACCGGGTTCAGATTTTGAAGGTGAATGACTCTT 520

Db 338 CGGTAACTCAGAGCTTTTAAATGATGAGATTCAGATTTTAAATGTTCTGACTCTTAT 397

QY 521 ATCAAGATATATCTTC-----ATTATCTTGAGGATTCCTTACAGATA 565

Db 398 ACAGGAATCTTTAGAGGCTCTGTGATGCTGAATTAAGAAATCTTAATTCGCTCTG 457

QY 566 AATCAATCTTAATAAACTGTGACGATTTAAAGCTTCCAGGACGAGGAAGAAAT 625

Db 458 AAGAACTCCGATCTGTTTGAATCGCCGACCTCAGAAATTTGATAGATTTTAAACCGAG 517

QY 626 TCACTAACTTTTACGAGGTCATTATCAAGACGAAAGCTGAATATTTATTTGCTTA 685

Db 518 GGTCTTTAAGCAATGAGGCTGTTAGTACGAAAAATGCCAAATTTATTTATTAACCT 577

QY 686 CGTATGCGAAGCTGCAAAATGTGATTTATTTACTATTTAAGGACGCGATTAAATATAAA 745

Db 578 CTTTGGACGCGTGCATTTTTCATTATTTACTACTAAGGAGTACTATAGATATGCA 637

QY 746 AAGAAATGGGAGTACTAGTGTGCAACCGTGTATCCAGGGTCAAGGAGAACTGATGTAAC 805

Db 638 CTAAATGGGGCTATACATATGCTACCTTTTAA-----ATTATCAAT 682

QY 806 AGCGTTTAAAGCGAAATTAAGAGTATATCTAATTTGTAGGGGTATTAACAAG 865

Db 683 CAAACTAGTAGAGCTTATGAACTATATCTGATTTATTCGTAATTTGTATATGAG 742

QY 866 GTTATAGTCAGATTAAGACGCGGCTCAAGTCTGAAGTTTGCGAAATTTATTAAT 925

Db 743 GTTCAACGAACTAAGACGAGGACGAGGACTAGTCTCAGCTTGTTAGAAATTCATGAT 802

QY 926 TTGCTAGAGAAATGACGTTGGCGGTATTTGATATTTATTTGCTATATTTCAACTATGAT 985

Db 803 ATCTTAGAGAGATGACATTTATGATTTATAGATATAGTATGATCATCTTCAAGCTTGATA 862

QY 986 TTGAAAAATATCCATTAGCAACAAGTGTAGAGTTAACTAGGAAATTTATACAGATCCAG 1045

Db 863 TTACTAATTAACCAATAGAAACAGATTTTCAGTTGAGTAGAGTCAATTATACAGATCCA 922

QY 1046 TGGGATATTCAGGGGAAATTATGTTGGAA 1077

Db 923 TTGGTTTGTACATCGTAGTAGTCTTAGGGGA 954

RESULT 15

BD128371 3471 bp DNA linear PAT 18-SEP-2002

LOCUS BD128371

DEFINITION Toxin active on Oestrinlanubialis.

ACCESSION BD128371.1 GI:23223316

VERSION JP 2002500166-A/42.

KEYWORDS

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 3471)

AUTHORS Schnepf, E.H., Wicker, C., Narva, K.E., Walz, M., Stockhoff, B.A. and Cohn, J.M.

TITLE Toxin active on Oestrinlanubialis

JOURNAL Patent: JP 2002500166-A 42 08-JAN-2002;

MYCOGEN CORP

COMMENT OS Unidentified

PN JP 2002500166-A/42

PD 08-JAN-2002 JP 2000526647

PF 15-DEC-1998 JP 2000526647

PI 31-DEC-1997 US 09/002285

PI ERNEST H SCHNEPF, CAROL WICKER, KENNETH E NARVA, MICHELE WALZ, PI BRIAN A STOCKHOF, JUDY MULLER COHN

PC A01N63/02//C07K14/325, C12N15/09, C12N15/00

Strandedness: Single;

CC Topology: Linear;

CC Toxin active on Oestrinlanubialis

FF Key Location/Qualifiers

FF source 1..3471

/organism="unidentified".

FEATURES

source 1..3471

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

ORIGIN

Query Match 8.0%; Score 172.4; DB 6; Length 3471;

Best Local Similarity 54.2%; Pred. No. 4.2e-22;

Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 287 GGGATCAGTCTCGATATAGTAACTATTTGGGACATCTTATCAATTCCTTGCTAGAAC 346

Db 158 GCATGACGAGAAAGAGCATATCTATTTGGGACACCATATGCTCTTATACACGAC 217

OY	347	CCGGATATGGGGAATCCCTGTAATATTT-----CAATAATAACAACCTATCCGT	400
Db	218	CTTCTCTTACTGGAATTAATTCCAAATGATATGACCTTATAGTAACTAGTAACCTACCTAGGAGTA	277
OY	401	CTTCGTCAATCTGTGGCAGACCTTCTATATGATTTATGATCTATATTCGTAAAG	460
Db	278	GTAAGGACATCCATATCAAGATTGTCTATATGACTTATATCTATTTATGATTTAC	337
OY	461	AGGTAGACGAGAGCCTGTTAAAGTACGAGGCTTGACAGATTTTGGAGTAAATGACTGCTT	520
Db	338	GGGTAAAGCAGAGTGTTTAAATGATGGAATGACGATTTTAATGTTCTGTACTCTTAT	397
OY	521	ATCAAGATTAATATCTC-----ATTATCTGAGGATTTGGCTTACAGATA	565
Db	398	ACAGGACCTATTTTAGAGGCTCTGTATGACTGTAATAAATCTTAATTTCTGCTTGTG	457
OY	566	AATCAAAATCTTAAAAAACTGTGTCAGTAGTAAACAGTTCACAGCACGGAGAAAGATY	625
Db	458	AAGAATCTCGTACTGTTTGAATGCGCACTAGAAATTTGATGAATTTTAACCCAG	517
OY	626	TCACTAAACTTTTACAGAGGTTCATTATCAAGACAGAACTGAATATTTATTTATGCTTA	685
Db	518	GGTCTTTAACGAATGTGGCTCGTTAGCTAGCAAAAAGCCCAATATTTATTTATCACTT	577
OY	686	CGTATGTCACAGCTGCAATGTCATTTATTACTATTTAAGGAGCGCACTTAAATTAATAA	745
Db	578	CTTTTGCGAGCGCTGCACTTTTTCATTTATTACTATAAGGAGATCTATGATATGGCA	637
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Db	638	CTAATTTGGGGGCTATACAAATGCTACACCTTTATATA-----ATTATCAAT	682
OY	806	AGCGTTTAAAGCGAAAAATAAAGATATCTAATATTTGTGTAGGGTGTATTAACAAG	865
Db	683	CAAAACTAGTAGAGCTTATGAACTATATTACTGATTATTGGTACATTGTATATATCAG	742
OY	866	GTTTATGATCAATTAAGACAGCGGGGTACAAGTCTGGAAGTTTGGTCGAAATTTATTAAT	925
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OY	926	TTTCGTAGAGAAATGACGTTGGCGATTTGGATATTAATTTGCTATATTTCCACTATAGAT	985
Db	803	ATCGTAGAGATGACATTTGATGTATTAGATTAGTACATCAATTTCCAGTCTTGGATA	862
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Db	863	TTACTAATTAACCATATGAAACAAGATTTTCAAGTTAGTAGAGGTCAATTTATACAGATCAA	922
OY	1046	TGGATATTTACAGGGGAAATTAATGTTGGGA	1077
Db	923	TTGGTTTGTATCATGTAGTAGTCTTAAGGGA	954

Search completed: December 19, 2005, 09:48:28
Job time : 7241.94 secs